

SEQUENCE LISTING

<110> APPLICANT: Ganymed Pharmaceuticals AG
 Sahin, Ugur
 Tureci, Oezlem
 Koslowski, Michael

<120> TITLE OF INVENTION: Genetic Products Differentially Expressed In Tumors And The Use Thereof

<130> FILE REFERENCE: 4883-0001

<140> CURRENT APPLICATION NUMBER: US/10/537,002

<141> CURRENT FILING DATE: 2005-05-20

<150> PRIOR APPLICATION NUMBER: PCT/EP2003/013091

<151> PRIOR FILING DATE: 2003-11-21

<150> PRIOR APPLICATION NUMBER: DE 102 54 601.0

<151> PRIOR FILING DATE: 2002-11-22

<160> NUMBER OF SEQ ID NOS: 141

<170> SOFTWARE: PatentIn version 3.1

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<211> LENGTH: 1875

<212> TYPE: DNA

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4883-0001 substitute.txt

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Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1      5      10      15
Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
20      25      30
Leu Gly Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
35      40      45
Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
50      55      60
Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65      70      75      80
Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
85      90      95
Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100     105     110
Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115     120     125
Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130     135     140
Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145     150     155     160
Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro
165     170     175
Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
180     185     190
Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
195     200     205
Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
210     215     220
Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
225     230     235     240
Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
245     250     255
Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
260     265     270
Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
275     280     285
Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu
290     295     300
Cys Val Thr Leu Ala
305
```

```
<210> SEQ ID NO 10
<211> LENGTH: 394
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 10
Met Thr Ala Gly Arg Ser Gln Glu Arg Arg Ala Gln Glu Met Gly Arg
1      5      10      15
Gly Ser Val Gln Gly Leu Asp Leu Lys Gly Asp Leu Glu Phe Phe Thr
20      25      30
Ala Pro Met Leu Ser Leu Arg Ser Phe Val Phe Val Gly Val Gly Ser
```

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      35      40      45
Gly Leu Thr Ser Ser His Ile Pro Ala Gln Arg Trp Ala Glu Trp Gly
  50      55      60
Gln Cys Leu Ala Pro Pro Ala Arg Ser Leu Leu Thr Ser Gly Ser Leu
  65      70      75      80
Cys Cys Pro Arg Thr Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser
      85      90      95
Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu
      100      105      110
Gly Val Leu Leu Val Leu Gly Leu Leu Asn Ser Leu Ala Leu Trp
      115      120      125
Val Phe Cys Cys Arg Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met
      130      135      140
Thr Asn Leu Ala Val Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe
      145      150      155      160
Val Leu His Ser Leu Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu
      165      170      175
Ser Gln Gly Ile Tyr Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val
      180      185      190
Thr Ala Ile Ala Val Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg
      195      200      205
Ala Arg Gly Leu Arg Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val
      210      215      220
Leu Trp Val Leu Val Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly
      225      230      235      240
Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn
      245      250      255
Ser Met Ala Phe Pro Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val
      260      265      270
Val Phe Cys Ser Leu Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro
      275      280      285
Thr Asp Val Gly Gln Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val
      290      295      300
Trp Ala Asn Leu Leu Val Phe Val Val Cys Phe Leu Pro Leu His Val
      305      310      315      320
Gly Leu Thr Val Arg Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu
      325      330      335
Glu Thr Ile Arg Arg Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala
      340      345      350
Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe
      355      360      365
Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys
      370      375      380
Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
      385      390

```

<210> SEQ ID NO 11

<211> LENGTH: 1073

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

```

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
  1      5      10      15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
      20      25      30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
      35      40      45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
      50      55      60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
      65      70      75      80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
      85      90      95

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Ser	Ser	Thr	Cys	Glu	Gly	Leu	Asp	Leu	Leu	Arg	Lys	Ile	Ser	Asn	Ala
			100					105					110		
Gln	Arg	Met	Gly	Cys	Val	Leu	Ile	Gly	Pro	Ser	Cys	Thr	Tyr	Ser	Thr
		115					120					125			
Phe	Gln	Met	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser	Ala
	130					135					140				
Gly	Ser	Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	Thr	Leu	Thr	Arg	Leu
145					150					155					160
Met	Ser	Pro	Ala	Arg	Lys	Leu	Met	Tyr	Phe	Leu	Val	Asn	Phe	Trp	Lys
				165					170					175	
Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Ser	Tyr	Val
			180					185					190		
Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	Asp	Cys	Phe	Trp	Tyr	Leu	Asn	Ala
		195					200					205			
Leu	Glu	Ala	Ser	Val	Ser	Tyr	Phe	Ser	His	Glu	Leu	Gly	Phe	Lys	Val
	210					215					220				
Val	Leu	Arg	Gln	Asp	Lys	Glu	Phe	Gln	Asp	Ile	Leu	Met	Asp	His	Asn
225					230					235					240
Arg	Lys	Ser	Asn	Val	Ile	Ile	Met	Cys	Gly	Gly	Pro	Glu	Phe	Leu	Tyr
			245						250					255	
Lys	Leu	Lys	Gly	Asp	Arg	Ala	Val	Ala	Glu	Asp	Ile	Val	Ile	Ile	Leu
			260					265					270		
Val	Asp	Leu	Phe	Asn	Asp	Gln	Tyr	Leu	Glu	Asp	Asn	Val	Thr	Ala	Pro
		275					280					285			
Asp	Tyr	Met	Lys	Asn	Val	Leu	Val	Leu	Thr	Leu	Ser	Pro	Gly	Asn	Ser
	290					295					300				
Leu	Leu	Asn	Ser	Ser	Phe	Ser	Arg	Asn	Leu	Ser	Pro	Thr	Lys	Arg	Asp
305					310					315					320
Phe	Ala	Leu	Ala	Tyr	Leu	Asn	Gly	Ile	Leu	Leu	Phe	Gly	His	Met	Leu
				325					330					335	
Lys	Ile	Phe	Leu	Glu	Asn	Gly	Glu	Asn	Ile	Thr	Thr	Pro	Lys	Phe	Ala
			340					345					350		
His	Ala	Phe	Arg	Asn	Leu	Thr	Phe	Glu	Gly	Tyr	Asp	Gly	Pro	Val	Thr
		355					360					365			
Leu	Asp	Asp	Trp	Gly	Asp	Val	Asp	Ser	Thr	Met	Val	Leu	Leu	Tyr	Thr
	370					375					380				
Ser	Val	Asp	Thr	Lys	Lys	Tyr	Lys	Val	Leu	Leu	Thr	Tyr	Asp	Thr	His
385					390					395					400
Val	Asn	Lys	Thr	Tyr	Pro	Val	Asp	Met	Ser	Pro	Thr	Phe	Thr	Trp	Lys
				405					410					415	
Asn	Ser	Lys	Leu	Pro	Asn	Asp	Ile	Thr	Gly	Arg	Gly	Pro	Gln	Ile	Leu
			420					425					430		
Met	Ile	Ala	Val	Phe	Thr	Leu	Thr	Gly	Ala	Val	Val	Leu	Leu	Leu	
		435					440					445			
Val	Ala	Leu	Leu	Met	Leu	Arg	Lys	Tyr	Arg	Lys	Asp	Tyr	Glu	Leu	Arg
	450					455					460				
Gln	Lys	Lys	Trp	Ser	His	Ile	Pro	Pro	Glu	Asn	Ile	Phe	Pro	Leu	Glu
465					470					475					480
Thr	Asn	Glu	Thr	Asn	His	Val	Ser	Leu	Lys	Ile	Asp	Asp	Asp	Lys	Arg
				485					490					495	
Arg	Asp	Thr	Ile	Gln	Arg	Leu	Arg	Gln	Cys	Lys	Tyr	Asp	Lys	Lys	Arg
			500					505					510		
Val	Ile	Leu	Lys	Asp	Leu	Lys	His	Asn	Asp	Gly	Asn	Phe	Thr	Glu	Lys
		515					520					525			
Gln	Lys	Ile	Glu	Leu	Asn	Lys	Leu	Leu	Gln	Ile	Asp	Tyr	Tyr	Asn	Leu
	530					535					540				
Thr	Lys	Phe	Tyr	Gly	Thr	Val	Lys	Leu	Asp	Thr	Met	Ile	Phe	Gly	Val
545					550					555					560
Ile	Glu	Tyr	Cys	Glu	Arg	Gly	Ser	Leu	Arg	Glu	Val	Leu	Asn	Asp	Thr
				565					570					575	
Ile	Ser	Tyr	Pro	Asp	Gly	Thr	Phe	Met	Asp	Trp	Glu	Phe	Lys	Ile	Ser
			580					585					590		
Val	Leu	Tyr	Asp	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	His	Ser	Ser	Lys

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      595      600      605
Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser
610
Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro
625
Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn
645
Ile Ser Gln Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu
660
Ile Ile Leu Arg Lys Glu Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg
675
Asn Glu Lys Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe
690
Arg Pro Asp Leu Phe Leu Glu Thr Ala Glu Glu Lys Glu Leu Glu Val
705
Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro
725
Asp Phe Lys Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe
740
His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu
755
Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln
770
Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu
785
Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu
805
Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly
820
Phe Thr Thr Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met
835
Leu Asn Asp Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp
850
Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly
865
Leu Pro Lys Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met
885
Ala Leu Glu Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu
900
Pro Gly Leu Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys
915
Ala Ala Gly Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly
930
Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
945
Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
965
Cys Gln Phe Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg
980
Gly Asn Glu Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe
995
Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln
1010
Ala Glu Phe Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln
1025
Ala Ala Gly Ile Arg Ser Gln Lys Pro Arg Arg Val Ala Ser Tyr
1040
Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
1055
Glu Ser Thr Tyr Phe
1070

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<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 12
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1      5      10      15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20     25     30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35     40     45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50     55     60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65     70     75     80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85     90     95
Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Pro
100    105    110

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<210> SEQ ID NO 13
<211> LENGTH: 258
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 13
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe Gln
1      5      10      15
Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn
20     25     30
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
35     40     45
Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
50     55     60
Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65     70     75     80
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
85     90     95
Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
100    105    110
Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
115    120    125
Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
130    135    140
Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
145    150    155    160
Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
165    170    175
Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
180    185    190
Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
195    200    205
Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
210    215    220
Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
225    230    235    240
Arg Lys Ser Asn Val Thr Ser Thr Trp Arg Thr Met Ser Gln Pro Leu
245    250    255
Thr Ile

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<210> SEQ ID NO 14
<211> LENGTH: 1070
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 14

```

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Met	Lys	Thr	Leu	Leu	Leu	Asp	Leu	Ala	Leu	Trp	Ser	Leu	Leu	Phe	Gln
1				5					10					15	
Pro	Gly	Trp	Leu	Ser	Phe	Ser	Ser	Gln	Val	Ser	Gln	Asn	Cys	His	Asn
			20					25					30		
Gly	Ser	Tyr	Glu	Ile	Ser	Val	Leu	Met	Met	Gly	Asn	Ser	Ala	Phe	Ala
		35					40					45			
Glu	Pro	Leu	Lys	Asn	Leu	Glu	Asp	Ala	Val	Asn	Glu	Gly	Leu	Glu	Ile
	50					55				60					
Val	Arg	Gly	Arg	Leu	Gln	Asn	Ala	Gly	Leu	Asn	Val	Thr	Val	Asn	Ala
65					70					75				80	
Thr	Phe	Met	Tyr	Ser	Asp	Gly	Leu	Ile	His	Asn	Ser	Gly	Asp	Cys	Arg
				85					90					95	
Ser	Ser	Thr	Cys	Glu	Gly	Leu	Asp	Leu	Leu	Arg	Lys	Ile	Ser	Asn	Ala
			100					105					110		
Gln	Arg	Met	Gly	Cys	Val	Leu	Ile	Gly	Pro	Ser	Cys	Thr	Tyr	Ser	Thr
		115					120					125			
Phe	Gln	Met	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser	Ala
	130					135					140				
Gly	Ser	Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	Thr	Leu	Thr	Arg	Leu
145					150					155					160
Met	Ser	Pro	Ala	Arg	Lys	Leu	Met	Tyr	Phe	Leu	Val	Asn	Phe	Trp	Lys
				165					170					175	
Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Ser	Tyr	Val
			180					185					190		
Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	Asp	Cys	Phe	Trp	Tyr	Leu	Asn	Ala
		195					200					205			
Leu	Glu	Ala	Ser	Val	Ser	Tyr	Phe	Ser	His	Glu	Leu	Gly	Phe	Lys	Val
	210					215					220				
Val	Leu	Arg	Gln	Asp	Lys	Glu	Phe	Gln	Asp	Ile	Leu	Met	Asp	His	Asn
225					230					235					240
Arg	Lys	Ser	Asn	Val	Ile	Ile	Met	Cys	Gly	Gly	Pro	Glu	Phe	Leu	Tyr
				245					250					255	
Lys	Leu	Lys	Gly	Asp	Arg	Ala	Val	Ala	Glu	Asp	Ile	Val	Ile	Ile	Leu
			260					265					270		
Val	Asp	Leu	Phe	Asn	Asp	Gln	Tyr	Leu	Glu	Asp	Asn	Val	Thr	Ala	Pro
		275					280					285			
Asp	Tyr	Met	Lys	Asn	Val	Leu	Val	Leu	Thr	Leu	Ser	Pro	Gly	Asn	Ser
	290					295					300				
Leu	Leu	Asn	Ser	Ser	Phe	Ser	Arg	Asn	Leu	Ser	Pro	Thr	Lys	Arg	Asp
305					310					315					320
Phe	Ala	Leu	Ala	Tyr	Leu	Asn	Gly	Ile	Leu	Leu	Phe	Gly	His	Met	Leu
				325					330					335	
Lys	Ile	Phe	Leu	Glu	Asn	Gly	Glu	Asn	Ile	Thr	Thr	Pro	Lys	Phe	Ala
			340					345					350		
His	Ala	Phe	Arg	Asn	Leu	Thr	Phe	Glu	Gly	Tyr	Asp	Gly	Pro	Val	Thr
		355					360					365			
Leu	Asp	Asp	Trp	Gly	Asp	Val	Asp	Ser	Thr	Met	Val	Leu	Leu	Tyr	Thr
	370					375					380				
Ser	Val	Asp	Thr	Lys	Lys	Tyr	Lys	Val	Leu	Leu	Thr	Tyr	Asp	Thr	His
385					390					395					400
Val	Asn	Lys	Thr	Tyr	Pro	Val	Asp	Met	Ser	Pro	Thr	Phe	Thr	Trp	Lys
				405					410					415	
Asn	Ser	Lys	Leu	Pro	Asn	Asp	Ile	Thr	Gly	Arg	Gly	Pro	Gln	Ile	Leu
			420					425					430		
Met	Ile	Ala	Val	Phe	Thr	Leu	Thr	Gly	Ala	Val	Val	Leu	Leu	Leu	
		435					440					445			
Val	Ala	Leu	Leu	Met	Leu	Arg	Lys	Tyr	Arg	Lys	Asp	Tyr	Glu	Leu	Arg
	450					455					460				
Gln	Lys	Lys	Trp	Ser	His	Ile	Pro	Pro	Glu	Asn	Ile	Phe	Pro	Leu	Glu
465					470					475					480
Thr	Asn	Glu	Thr	Asn	His	Val	Ser	Leu	Lys	Ile	Asp	Asp	Asp	Lys	Arg
				485					490					495	
Arg	Asp	Thr	Ile	Gln	Arg	Leu	Arg	Gln	Cys	Lys	Tyr	Asp	Lys	Lys	Arg

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			500					505					510				
Val	Ile	Leu	Lys	Asp	Leu	Lys	His	Asn	Asp	Gly	Asn	Phe	Thr	Glu	Lys		
		515					520					525					
Gln	Lys	Ile	Glu	Leu	Asn	Lys	Ile	Asp	Tyr	Tyr	Asn	Leu	Thr	Lys	Phe		
	530					535					540						
Tyr	Gly	Thr	Val	Lys	Leu	Asp	Thr	Met	Ile	Phe	Gly	Val	Ile	Glu	Tyr		
545					550					555				560			
Cys	Glu	Arg	Gly	Ser	Leu	Arg	Glu	Val	Leu	Asn	Asp	Thr	Ile	Ser	Tyr		
				565					570					575			
Pro	Asp	Gly	Thr	Phe	Met	Asp	Trp	Glu	Phe	Lys	Ile	Ser	Val	Leu	Tyr		
			580					585					590				
Asp	Ile	Ala	Lys	Gly	Met	Ser	Tyr	Leu	His	Ser	Ser	Lys	Thr	Glu	Val		
		595					600					605					
His	Gly	Arg	Leu	Lys	Ser	Thr	Asn	Cys	Val	Val	Asp	Ser	Arg	Met	Val		
	610					615					620						
Val	Lys	Ile	Thr	Asp	Phe	Gly	Cys	Asn	Ser	Ile	Leu	Pro	Pro	Lys	Lys		
625					630					635				640			
Asp	Leu	Trp	Thr	Ala	Pro	Glu	His	Leu	Arg	Gln	Ala	Asn	Ile	Ser	Gln		
				645					650					655			
Lys	Gly	Asp	Val	Tyr	Ser	Tyr	Gly	Ile	Ile	Ala	Gln	Glu	Ile	Ile	Leu		
			660					665					670				
Arg	Lys	Glu	Thr	Phe	Tyr	Thr	Leu	Ser	Cys	Arg	Asp	Arg	Asn	Glu	Lys		
		675					680					685					
Ile	Phe	Arg	Val	Glu	Asn	Ser	Asn	Gly	Met	Lys	Pro	Phe	Arg	Pro	Asp		
	690					695					700						
Leu	Phe	Leu	Glu	Thr	Ala	Glu	Glu	Lys	Glu	Leu	Glu	Val	Tyr	Leu	Leu		
705					710					715				720			
Val	Lys	Asn	Cys	Trp	Glu	Glu	Asp	Pro	Glu	Lys	Arg	Pro	Asp	Phe	Lys		
				725					730					735			
Lys	Ile	Glu	Thr	Leu	Ala	Lys	Ile	Phe	Gly	Leu	Phe	His	Asp	Gln			
			740				745					750					
Lys	Asn	Glu	Ser	Tyr	Met	Asp	Thr	Leu	Ile	Arg	Arg	Leu	Gln	Leu	Tyr		
		755					760					765					
Ser	Arg	Asn	Leu	Glu	His	Leu	Val	Glu	Glu	Arg	Thr	Gln	Leu	Tyr	Lys		
	770					775					780						
Ala	Glu	Arg	Asp	Arg	Ala	Asp	Arg	Leu	Asn	Phe	Met	Leu	Leu	Pro	Arg		
785					790					795				800			
Leu	Val	Val	Lys	Ser	Leu	Lys	Glu	Lys	Gly	Phe	Val	Glu	Pro	Glu	Leu		
				805					810					815			
Tyr	Glu	Glu	Val	Thr	Ile	Tyr	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr	Thr		
			820					825					830				
Ile	Cys	Lys	Tyr	Ser	Thr	Pro	Met	Glu	Val	Val	Asp	Met	Leu	Asn	Asp		
		835					840					845					
Ile	Tyr	Lys	Ser	Phe	Asp	His	Ile	Val	Asp	His	His	Asp	Val	Tyr	Lys		
	850					855					860						
Val	Glu	Thr	Ile	Gly	Asp	Ala	Tyr	Met	Val	Ala	Ser	Gly	Leu	Pro	Lys		
865					870					875				880			
Arg	Asn	Gly	Asn	Arg	His	Ala	Ile	Asp	Ile	Ala	Lys	Met	Ala	Leu	Glu		
				885					890					895			
Ile	Leu	Ser	Phe	Met	Gly	Thr	Phe	Glu	Leu	Glu	His	Leu	Pro	Gly	Leu		
			900					905					910				
Pro	Ile	Trp	Ile	Arg	Ile	Gly	Val	His	Ser	Gly	Pro	Cys	Ala	Ala	Gly		
		915					920					925					
Val	Val	Gly	Ile	Lys	Met	Pro	Arg	Tyr	Cys	Leu	Phe	Gly	Asp	Thr	Val		
	930					935					940						
Asn	Thr	Ala	Ser	Arg	Met	Glu	Ser	Thr	Gly	Leu	Pro	Leu	Arg	Ile	His		
945					950					955				960			
Val	Ser	Gly	Ser	Thr	Ile	Ala	Ile	Leu	Lys	Arg	Thr	Glu	Cys	Gln	Phe		
				965					970					975			
Leu	Tyr	Glu	Val	Arg	Gly	Glu	Thr	Tyr	Leu	Lys	Gly	Arg	Gly	Asn	Glu		
			980					985					990				
Thr	Thr	Tyr	Trp	Leu	Thr	Gly	Met	Lys	Asp	Gln	Lys	Phe	Asn	Leu	Pro		
		995					1000					1005					

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Thr Pro  Pro Thr Val Glu Asn  Gln Gln Arg Leu Gln  Ala Glu Phe
1010                               1015           1020
Ser Asp  Met Ile Ala Asn Ser   Leu Gln Lys Arg Gln  Ala Ala Gly
1025                               1030           1035
Ile Arg  Ser Gln Lys Pro Arg   Arg Val Ala Ser Tyr  Lys Lys Gly
1040                               1045           1050
Thr Leu  Glu Tyr Leu Gln Leu   Asn Thr Thr Asp Lys  Glu Ser Thr
1055                               1060           1065
Tyr Phe
1070

```

<210> SEQ ID NO 15

<211> LENGTH: 93

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

```

Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
1      5      10
Tyr Ser Ala Thr Ala Lys Leu Ile Asn Lys Cys Pro Leu Pro Val Asp
20      25      30
Lys Leu Ala Pro Leu Pro Leu Asp Asn Ile Leu Pro Phe Met Asp Pro
35      40      45
Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
50      55      60
Glu Gly Leu Arg Lys Cys Val Asn Glu Leu Gly Pro Glu Ala Ser Glu
65      70      75      80
Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
85      90

```

<210> SEQ ID NO 16

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

```

Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
1      5      10
Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr
20      25      30
Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln Gly
35      40      45
Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly Phe Thr Glu Cys Arg
50      55      60
Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100      105      110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115      120      125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130      135      140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145      150      155      160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165      170      175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180      185      190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195      200      205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210      215      220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile

```

225 Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
230
235
240
245
250
255
260

```
<210> SEQ ID NO 17
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 17
      Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn
       1                               5             10
```

```
<210> SEQ ID NO 18
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 18
      Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln
       1                5                10
```

```

<210> SEQ ID NO 19
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 19
Met Ala Val Thr Ala Cys Gln Gly Leu Gly Phe Val Val Ser Leu Ile
 1          5          10          15
Gly Ile Ala Gly Ile Ile Ala Ala Thr Cys Met Asp Gln Trp Ser Thr
          20          25          30
Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe Asn Tyr Gln
          35          40          45

```

```
<210> SEQ ID NO 20
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 20
      aggtacatga gcatcagcct g                                     21
```

```
<210> SEQ ID NO 21
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 21
gcagcagttg gcacctgaga g
```

```

<210> SEQ ID NO 22
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 22
      gcaatagaca ttgccaagat g

```

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```

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 23
aacgctgttg attctccaca g                                     21

<210> SEQ ID NO 24
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 24
ggatcctcct ttagttccca ggtgagtcag aac                       33

<210> SEQ ID NO 25
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 25
tgctctggag gctagcgttt c                                     21

<210> SEQ ID NO 26
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 26
accaatcatg ttagcctcaa g                                     21

<210> SEQ ID NO 27
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 27
agctatggga tcatgcaca g                                     21

<210> SEQ ID NO 28
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 28
cctttgagct ggagcatctt c                                     21

<210> SEQ ID NO 29
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 29
ctttctagct ggagacatca g                                     21

<210> SEQ ID NO 30
<211> LENGTH: 21

```

```

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 30
caccatggta ctgtcaacat c                                     21

<210> SEQ ID NO 31
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 31
atgtcataca agacagagat c                                     21

<210> SEQ ID NO 32
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 32
tctgccttgt acagcttgtt c                                     21

<210> SEQ ID NO 33
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 33
tctgtggtat tcagctgcaa g                                     21

<210> SEQ ID NO 34
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 34
tactcaggaa aatttcacct tg                                    22

<210> SEQ ID NO 35
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 35
gaccacaaca ggaaaagcaa tgtgacc                               27

<210> SEQ ID NO 36
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 36
gatagaattg aacaagattg ac                                    22

<210> SEQ ID NO 37
<211> LENGTH: 21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 37
cagcctttgt agttactctg c
21

<210> SEQ ID NO 38
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 38
tgtcacacca agtgtgatag c
21

<210> SEQ ID NO 39
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 39
ggttcgtggt ttcactgatt gggattgc
28

<210> SEQ ID NO 40
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
<400> SEQUENCE: 40
cggctttgta gttggtttct tctggtg
27

<210> SEQ ID NO 41
<211> LENGTH: 3814
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 41
ctattgaagc cacctgctca ggacaatgaa attcttcagt tacattctgg tttatcgccg 60
atttctcttc gtggttttca ctgtgttggt tttactacct ctgcccacac tcctccacac 120
caaggaagca gaatgtgcct acacactctt tgtggtcgcc acattttggc tcacagaagc 180
attgcctctg tcggtaacag ctttgctacc tagtttaatg ttacccatgt ttgggatcat 240
gaccttctaag aaggtggcat ctgcttattt caaggatttt cacttactgc taattggagt 300
tatctgttta gcaacatcca tagaaaaatg gaatttgcac aagagaattg ctctgaaaat 360
ggtgatgatg gttggtgtaa atcctgcacg gctgacgctg gggttcatga gcagcactgc 420
ctttttgtct atgtggctca gcaacacctc gacggctgcc atgggtgatgc ccattgcgga 480
ggctgtagtg cagcagatca tcaatgcaga agcagaggtc gaggccactc agatgactta 540
cttcaacgga tcaaccaacc acggactaga aattgatgaa agtggttaatg gacatgaaat 600
aaatgagagg aaagagaaaa caaaaccagt tccaggatac aataatgata cagggaaaaat 660
ttcaagcaag gtggagttgg aaaagaactc aggcattgaga accaaatatc gaacaaagaa 720
gggccacgtg acacgtaaac ttacgtgttt gtgcattgcc tactcttcta ccattggtgg 780
actgacaaca atcactggta cctccaccaa cttgatcttt gcagagtatt tcaatacacg 840
ctatcctgac tgtcgttgcc tcaacttttg atcatggttt acgttttcct tcccagctgc 900
ccttatcatt ctactcttat cctggatctg gcttcagtgg cttttcctag gattcaattt 960
taaggagatg ttcaaatgtg gcaaaaccaa aacagtccaa caaaaagctt gtgctgaggt 1020
gattaagcaa gaatacacia agcttgggcc aataaggatg caagaaattg tgacccttgg 1080
cctcttcatt ataatggctc tgctatggtt tagtcgagac cccggatttg ttcctggttg 1140
gtctgcactt ttttcagagt accctgggtt tgctacagat tcaactgttg ctttacttat 1200
agggctgcta ttctttctta tcccagctaa gacactgact aaaactacac ctacaggaga 1260
aattgttgct ttgattact ctccactgat tacttgaaa gaattccagt cattcatgcc 1320
ctgggatata gccattcttg ttggtggagg gtttgccctg gcagatgggt gtgaggagtc 1380
tggattatct aagtggatag gaaataaatt atctcctctg ggttcattac cagcatggct 1440

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aataattctg	atatcttctt	tgatggtgac	atctttaact	gaggtagcca	gcaatccagc	1500
taccattaca	ctcttttctc	caatattatc	tccattggcc	gaagccattc	atgtgaaccc	1560
tctttatatt	ctgatacctt	ctactctgtg	tacttcattt	gcattccctc	taccagtagc	1620
aaatccaccc	aagtctattg	tcttttcata	tggtcatctg	aaagtcattg	acatgggttaa	1680
agctggactt	ggtgtcaaca	ttgttgggtg	tgctgtggtt	atgcttggca	tatgtacttg	1740
gattgtaccc	atgtttgacc	tctacactta	cccttcgtgg	gctcctgcta	tgagtaatga	1800
gaccatgcca	taataagcac	aaaatttctg	actatcttgc	ggtaatttct	ggaagacatt	1860
aatgattgac	tgtaaaatgt	ggctctaaat	aactaatgac	acacatttaa	atcagttatg	1920
gtgtagctgc	tgcaattccc	gtgaataccc	gaaacctgct	ggtataactc	agagtcacata	1980
tttgttattg	cagtgaact	aaagagcatc	tatgtgcctt	catcaagaag	cccatgtttt	2040
gagatttttg	tcatgaacca	tctgcaactt	gcttcacatc	aagaataatt	tataacttga	2100
ccttcaaaga	gattagagca	tttgtttcat	cttacagttg	gagttcaatg	taacatttta	2160
aatgcaattt	attatttcag	aaatttccca	tgaaactaaa	aatagaaaat	aagatataca	2220
agttaattcg	gtacttggat	aaatcatttc	tgcattgttg	ttccagagaa	tttgctgaga	2280
aatcaaagcc	atggtcatct	ggtgatgaag	agaaaagggt	aatctaaatg	atatgtgcat	2340
ttcctcattt	aaaaaatcca	attggattat	tcttaatata	tacatgtaat	atgaaaattg	2400
agattgaagc	actaattcca	aaattatggc	tgaatatact	aaataacaga	aaagttagag	2460
ataagaattt	atttctactg	aactctatag	ttagtgtaat	ataattcata	tttttatgat	2520
attggcacac	tgagaaattc	attttgtaga	gctatggata	aggcttgcta	tgatttgcac	2580
tattagtaca	gtatagttag	aaaggaaaag	tgaacactat	aaaactatta	acatattttc	2640
gtatatgagt	aacaactttg	cttaagtgtt	tatcttagtt	cagaaatata	taatgtcata	2700
tgttaaaaat	aaagagatgt	agaaatctaa	atgaattatc	actgtgtata	cagacagaaa	2760
aatcacataa	ctctgggtgtg	ttaacattgc	aatgaaaaaa	tgaaaaaaag	aaggaaaaaa	2820
gaataagaat	gaaaactgct	gacgtattac	aaaacagaaa	aataaatgat	ttaaaaatcaa	2880
atcaaaaaga	aaaaaactaa	acattttaaac	aaaaatggga	taagaatagt	cttctagaag	2940
tgaggatgcg	taaaagaatg	agtttccaat	taccctgatg	tgacaattac	acattgtaga	3000
caggtagcaa	aatatcacat	acacccccaa	aatatgtaca	aatattatat	atcaataaat	3060
aaatttttaa	agagtaagtg	ctattggcat	tccaaaattc	agctaaagga	aaaatgatca	3120
aaaacaaagt	aaggtgcaca	gtttagcaaaa	gatgcagatg	ttatatcaca	gcaattctca	3180
tgctaaaaat	acaacaaaag	acaaagcaaa	aaataaacct	ttgctttttt	tttttttttt	3240
tttttttttt	gagacggagt	ctcgctctgt	cgcccaggct	ggagtgcagt	ggcgggatct	3300
cggctcactg	caagctccgc	ctcccagggt	cacgccattc	tcctgcctca	gccaaacctt	3360
tgctattttt	aatcttcgtt	ggcactttcc	agctgttact	gacctgtgca	ttttttgttc	3420
aaataagatt	atttacaaac	ttattcttga	aactaaatat	agtaaagagg	gtttttaaaa	3480
taatatttaa	catacgaatt	attaattggc	catgttcatt	atztatctat	gtttattaat	3540
gggccaatgc	aaaaaatcat	tttttcaaag	aaaaatttgt	ccatgtaaag	cttaaattat	3600
aatattgctg	ctttgtataa	ctcttctatg	tttattctat	tcatttgttc	ctttccctac	3660
catattttac	acatgtattt	ataatctgtg	gtattttatta	catttctgct	tttttctagt	3720
cattcaattt	atcactgctg	aattgcatca	gatcatggat	gcatttttat	tatgaaaaaa	3780
taaaatgact	tttcaaatta	aaaaaaaaaa	aaaa			3814

<210> SEQ ID NO 42

<211> LENGTH: 734

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

caggacaatg	aaattcttca	gttacattct	ggtttatcgc	cgatttctct	tcgtggtttt	60
cactgtgttg	gttttactac	ctctgcccc	cgtcctccac	accaaggaag	cagaatgtgc	120
ctacacactc	tttgtggtcg	ccacattttg	gctcacagaa	gcattgcctc	tgctcggtaac	180
agcttttgcta	cctagtttaa	tgttacccat	gtttgggata	atgccttcta	agaaggtggc	240
atctgcttat	ttcaaggatt	ttcacttact	gctaattgga	gttatctgtt	tagcaacatc	300
catagaaaaa	tggaatttgc	acaagagaa	tgctctgaaa	atgggtgatga	tggttgggtg	360
aaatcctgca	tggtctgacg	tggtgttcat	gagcagcact	gcctttttgt	ctatgtggct	420
cagcaacacc	tcgacggctg	ccatggtgat	gccatttgcg	gaggctgtag	tgacgcagat	480
catcaatgca	gaagcagagg	tcgaggccac	tcagatgact	tacttcaacg	gatcaaccaa	540
ccacggacta	gaaatttgatg	aaagtgttaa	tgacatgaa	ataaatgaga	ggaaagagaa	600
aacaaaacca	gttccaggat	acaataatga	tacagggaaa	atttcaagca	aggtggagtt	660
ggaaaagact	gtttaactac	tgaaatgaag	ctatttctct	gactaaacat	aactgaaaaa	720
ccattcatta	aatg					734

<210> SEQ ID NO 43

<211> LENGTH: 539

<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

gccactcaga	tgacttactt	caacggatca	accaaccacg	gactagaaat	tgatgaaagt	60
gttaatggac	atgaaataaa	tgagaggaaa	gagaaaacaa	aaccagttcc	aggatacaat	120
aatgatacag	ggaaaatttc	aagcaagggtg	gagttggaaa	agcactggaa	acttgcagtt	180
caagatggct	ccccatctcc	ctctgtccat	tctgtatcgc	agctagctgc	tcaaggaaag	240
gagaaagtgg	aaggcatatg	tacttagaaa	ttattctatt	actttcctgg	atttaagagt	300
attcagattt	tctattttcaa	catcaaacaa	ttgcattttt	aaaaagaaat	ttatgtgttc	360
catgtcaa	at	ttagtagtgt	gtggttgttt	ataatatttt	cttatatcta	420
atagtat	ttta	tagttatatg	tctttatttc	taacattttt	cttgtgcttt	480
ttaaagatta	tttttaata	atcttttattt	catttaata	aaatatttta	tttaagtc	539

<210> SEQ ID NO 44

<211> LENGTH: 556

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

cacggactag	aaattgatga	aagtgttaat	ggacatgaaa	taaatgagag	gaaagagaaa	60
acaaaaccag	ttccaggata	caataatgat	acagggaaaa	tttcaagcaa	ggtggagttg	120
gaaaagaact	caggcatgag	aaccaaatat	cgaacaaaga	agggccacgt	gacacgtaaa	180
cttacgtgtt	tgtgcattgc	ctactcttct	accattgggtg	gactgacaac	aatcactggg	240
acctccacca	acttgatctt	tgcagagtat	ttcaatacat	tccatccaca	cagaagagga	300
gatcgtacaa	ggcatgtaca	ccaggaggca	gaaatttgag	gcatactctg	gaactctgtc	360
taccacatcc	tgaacatcac	acagtttcca	ctcttggtgc	cttcaatcct	gagaatgcat	420
ccaggagcca	ttctgtttta	tgtcaattac	taattagatc	atgtcacggt	actaacttac	480
tacgttccaa	ttagtcctta	ttgcatttgt	aataaaatcc	gcatactttc	ggactggcta	540
caaggttata	catgat					556

<210> SEQ ID NO 45

<211> LENGTH: 595

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

Met	Lys	Phe	Phe	Ser	Tyr	Ile	Leu	Val	Tyr	Arg	Arg	Phe	Leu	Phe	Val	
1				5					10					15		
Val	Phe	Thr	Val	Leu	Val	Leu	Leu	Pro	Leu	Pro	Ile	Val	Leu	His	Thr	
			20					25					30			
Lys	Glu	Ala	Glu	Cys	Ala	Tyr	Thr	Leu	Phe	Val	Val	Ala	Thr	Phe	Trp	
		35					40					45				
Leu	Thr	Glu	Ala	Leu	Pro	Leu	Ser	Val	Thr	Ala	Leu	Leu	Pro	Ser	Leu	
		50				55					60					
Met	Leu	Pro	Met	Phe	Gly	Ile	Met	Pro	Ser	Lys	Lys	Val	Ala	Ser	Ala	
65				70					75					80		
Tyr	Phe	Lys	Asp	Phe	His	Leu	Leu	Leu	Ile	Gly	Val	Ile	Cys	Leu	Ala	
			85						90					95		
Thr	Ser	Ile	Glu	Lys	Trp	Asn	Leu	His	Lys	Arg	Ile	Ala	Leu	Lys	Met	
			100					105					110			
Val	Met	Met	Val	Gly	Val	Asn	Pro	Ala	Trp	Leu	Thr	Leu	Gly	Phe	Met	
		115					120					125				
Ser	Ser	Thr	Ala	Phe	Leu	Ser	Met	Trp	Leu	Ser	Asn	Thr	Ser	Thr	Ala	
		130				135					140					
Ala	Met	Val	Met	Pro	Ile	Ala	Glu	Ala	Val	Val	Gln	Gln	Ile	Ile	Asn	
145				150					155					160		
Ala	Glu	Ala	Glu	Val	Glu	Ala	Thr	Gln	Met	Thr	Tyr	Phe	Asn	Gly	Ser	
			165					170						175		
Thr	Asn	His	Gly	Leu	Glu	Ile	Asp	Glu	Ser	Val	Asn	Gly	His	Glu	Ile	
			180				185						190			
Asn	Glu	Arg	Lys	Glu	Lys	Thr	Lys	Pro	Val	Pro	Gly	Tyr	Asn	Asn	Asp	
		195					200				205					
Thr	Gly	Lys	Ile	Ser	Ser	Lys	Val	Glu	Leu	Glu	Lys	Asn	Ser	Gly	Met	
	210					215					220					
Arg	Thr	Lys	Tyr	Arg	Thr	Lys	Lys	Gly	His	Val	Thr	Arg	Lys	Leu	Thr	
225				230					235						240	

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Cys	Leu	Cys	Ile	Ala	Tyr	Ser	Ser	Thr	Ile	Gly	Gly	Leu	Thr	Thr	Ile
				245					250					255	
Thr	Gly	Thr	Ser	Thr	Asn	Leu	Ile	Phe	Ala	Glu	Tyr	Phe	Asn	Thr	Arg
			260					265					270		
Tyr	Pro	Asp	Cys	Arg	Cys	Leu	Asn	Phe	Gly	Ser	Trp	Phe	Thr	Phe	Ser
		275					280					285			
Phe	Pro	Ala	Ala	Leu	Ile	Ile	Leu	Leu	Leu	Ser	Trp	Ile	Trp	Leu	Gln
	290					295					300				
Trp	Leu	Phe	Leu	Gly	Phe	Asn	Phe	Lys	Glu	Met	Phe	Lys	Cys	Gly	Lys
305					310				315					320	
Thr	Lys	Thr	Val	Gln	Gln	Lys	Ala	Cys	Ala	Glu	Val	Ile	Lys	Gln	Glu
				325					330					335	
Tyr	Gln	Lys	Leu	Gly	Pro	Ile	Arg	Tyr	Gln	Glu	Ile	Val	Thr	Leu	Val
			340					345					350		
Leu	Phe	Ile	Ile	Met	Ala	Leu	Leu	Trp	Phe	Ser	Arg	Asp	Pro	Gly	Phe
		355					360					365			
Val	Pro	Gly	Trp	Ser	Ala	Leu	Phe	Ser	Glu	Tyr	Pro	Gly	Phe	Ala	Thr
	370					375					380				
Asp	Ser	Thr	Val	Ala	Leu	Leu	Ile	Gly	Leu	Leu	Phe	Phe	Leu	Ile	Pro
385					390				395						400
Ala	Lys	Thr	Leu	Thr	Lys	Thr	Thr	Pro	Thr	Gly	Glu	Ile	Val	Ala	Phe
				405					410					415	
Asp	Tyr	Ser	Pro	Leu	Ile	Thr	Trp	Lys	Glu	Phe	Gln	Ser	Phe	Met	Pro
			420					425					430		
Trp	Asp	Ile	Ala	Ile	Leu	Val	Gly	Gly	Gly	Phe	Ala	Leu	Ala	Asp	Gly
		435					440					445			
Cys	Glu	Glu	Ser	Gly	Leu	Ser	Lys	Trp	Ile	Gly	Asn	Lys	Leu	Ser	Pro
	450					455					460				
Leu	Gly	Ser	Leu	Pro	Ala	Trp	Leu	Ile	Ile	Leu	Ile	Ser	Ser	Leu	Met
465					470					475					480
Val	Thr	Ser	Leu	Thr	Glu	Val	Ala	Ser	Asn	Pro	Ala	Thr	Ile	Thr	Leu
				485					490					495	
Phe	Leu	Pro	Ile	Leu	Ser	Pro	Leu	Ala	Glu	Ala	Ile	His	Val	Asn	Pro
			500					505					510		
Leu	Tyr	Ile	Leu	Ile	Pro	Ser	Thr	Leu	Cys	Thr	Ser	Phe	Ala	Phe	Leu
		515					520					525			
Leu	Pro	Val	Ala	Asn	Pro	Pro	Asn	Ala	Ile	Val	Phe	Ser	Tyr	Gly	His
	530					535					540				
Leu	Lys	Val	Ile	Asp	Met	Val	Lys	Ala	Gly	Leu	Gly	Val	Asn	Ile	Val
545					550					555					560
Gly	Val	Ala	Val	Val	Met	Leu	Gly	Ile	Cys	Thr	Trp	Ile	Val	Pro	Met
				565					570					575	
Phe	Asp	Leu	Tyr	Thr	Tyr	Pro	Ser	Trp	Ala	Pro	Ala	Met	Ser	Asn	Glu
			580					585					590		
Thr	Met	Pro													
		595													

<210> SEQ ID NO 46

<211> LENGTH: 224

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

Arg	Thr	Met	Lys	Phe	Phe	Ser	Tyr	Ile	Leu	Val	Tyr	Arg	Arg	Phe	Leu
1				5					10					15	
Phe	Val	Val	Phe	Thr	Val	Leu	Val	Leu	Leu	Pro	Leu	Pro	Ile	Val	Leu
			20					25					30		
His	Thr	Lys	Glu	Ala	Glu	Cys	Ala	Tyr	Thr	Leu	Phe	Val	Val	Ala	Thr
		35					40					45			
Phe	Trp	Leu	Thr	Glu	Ala	Leu	Pro	Leu	Ser	Val	Thr	Ala	Leu	Leu	Pro
	50					55					60				
Ser	Leu	Met	Leu	Pro	Met	Phe	Gly	Ile	Met	Pro	Ser	Lys	Lys	Val	Ala
65					70					75					80
Ser	Ala	Tyr	Phe	Lys	Asp	Phe	His	Leu	Leu	Ile	Gly	Val	Ile	Cys	

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				85					90					95			
Leu	Ala	Thr	Ser	Ile	Glu	Lys	Trp	Asn	Leu	His	Lys	Arg	Ile	Ala	Leu		
			100					105					110				
Lys	Met	Val	Met	Met	Val	Gly	Val	Asn	Pro	Ala	Trp	Leu	Thr	Leu	Gly		
		115					120					125					
Phe	Met	Ser	Ser	Thr	Ala	Phe	Leu	Ser	Met	Trp	Leu	Ser	Asn	Thr	Ser		
	130					135				140							
Thr	Ala	Ala	Met	Val	Met	Pro	Ile	Ala	Glu	Ala	Val	Val	Gln	Gln	Ile		
145					150				155						160		
Ile	Asn	Ala	Glu	Ala	Glu	Val	Glu	Ala	Thr	Gln	Met	Thr	Tyr	Phe	Asn		
			165					170						175			
Gly	Ser	Thr	Asn	His	Gly	Leu	Glu	Ile	Asp	Glu	Ser	Val	Asn	Gly	His		
			180					185					190				
Glu	Ile	Asn	Glu	Arg	Lys	Glu	Lys	Thr	Lys	Pro	Val	Pro	Gly	Tyr	Asn		
		195				200				205							
Asn	Asp	Thr	Gly	Lys	Ile	Ser	Ser	Lys	Val	Glu	Leu	Glu	Lys	Thr	Val		
	210					215				220							

<210> SEQ ID NO 47

<211> LENGTH: 88

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

Ala	Thr	Gln	Met	Thr	Tyr	Phe	Asn	Gly	Ser	Thr	Asn	His	Gly	Leu	Glu		
1				5				10					15				
Ile	Asp	Glu	Ser	Val	Asn	Gly	His	Glu	Ile	Asn	Glu	Arg	Lys	Glu	Lys		
			20					25				30					
Thr	Lys	Pro	Val	Pro	Gly	Tyr	Asn	Asn	Asp	Thr	Gly	Lys	Ile	Ser	Ser		
		35					40				45						
Lys	Val	Glu	Leu	Glu	Lys	His	Trp	Lys	Leu	Ala	Val	Gln	Asp	Gly	Ser		
	50					55				60							
Pro	Ser	Pro	Ser	Val	His	Ser	Val	Ser	Gln	Leu	Ala	Ala	Gln	Gly	Lys		
65					70				75						80		
Glu	Lys	Val	Glu	Gly	Ile	Cys	Thr										
				85													

<210> SEQ ID NO 48

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

His	Gly	Leu	Glu	Ile	Asp	Glu	Ser	Val	Asn	Gly	His	Glu	Ile	Asn	Glu		
1				5				10					15				
Arg	Lys	Glu	Lys	Thr	Lys	Pro	Val	Pro	Gly	Tyr	Asn	Asn	Asp	Thr	Gly		
			20					25				30					
Lys	Ile	Ser	Ser	Lys	Val	Glu	Leu	Glu	Lys	Asn	Ser	Gly	Met	Arg	Thr		
		35				40				45							
Lys	Tyr	Arg	Thr	Lys	Lys	Gly	His	Val	Thr	Arg	Lys	Leu	Thr	Cys	Leu		
	50					55				60							
Cys	Ile	Ala	Tyr	Ser	Ser	Thr	Ile	Gly	Gly	Leu	Thr	Thr	Ile	Thr	Gly		
65				70					75						80		
Thr	Ser	Thr	Asn	Leu	Ile	Phe	Ala	Glu	Tyr	Phe	Asn	Thr	Phe	His	Pro		
			85					90					95				
His	Arg	Arg	Gly	Asp	Arg	Thr	Arg	His	Val	His	Gln	Glu	Ala	Glu	Ile		
			100					105					110				

<210> SEQ ID NO 49

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide

<400> SEQUENCE: 49

ccagctttaa ccatgtcaat g

21

<210> SEQ ID NO 50
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 50
 cagatgggtg tgaggagtct g

21

<210> SEQ ID NO 51
 <211> LENGTH: 3311
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 51

tgctaattgct	tttggtacaa	atggatgtgg	aatataattg	aatattttct	tgtttaagg	60
gagcatgaag	aggtggtgag	gttatgtcaa	gcatctggca	cagctgaagg	cagatggaaa	120
tatttacaag	tacgcaattt	gagactaaga	tattgttatc	attctcctat	tgaagacaag	180
agcaatagta	aaacacatca	ggtcaggggg	ttaaagacct	gtgataaacc	acttccgata	240
agttggaac	gtgtgtctat	attttcatat	ctgtatatat	ataatggtaa	agaaagacac	300
cttcgtaacc	cgcattttcc	aaagagagga	atcacagggg	gatgtacagc	aatggggcca	360
tttaagagtt	ctgtgttcat	cttgattctt	caccttctag	aagggggcct	gagtaattca	420
ctcattcagc	tgaacaacaa	tggtctatgaa	ggcattgtcg	ttgcaatcga	ccccaatgtg	480
ccagaagatg	aaacactcat	tcaacaaata	aaggacatgg	tgaccagagg	atctctgtat	540
ctgtttgaag	ctacaggaaa	gcgattttat	ttcaaaaatg	ttgccatttt	gattcctgaa	600
acatggaaga	caaaggctga	ctatgtgaga	ccaaaacttg	agacctacaa	aaatgctgat	660
gttctgggtg	ctgagtctac	tcctccaggt	aatgatgaac	cctacactga	gcagatgggc	720
aactgtggag	agaagggtga	aaggatccac	ctcactcctg	atttcattgc	aggaaaaaag	780
ttagctgaat	atggaccaca	aggtaaggca	tttgtccatg	agtgggctca	tctacgatgg	840
ggagtatttg	acgagtacaa	taatgatgag	aaattctact	tatccaatgg	aagaatacaa	900
gcagtaagat	gttcagcagg	tattactggt	acaaatgtag	taaagaagtg	tcaggagggc	960
agctgtttaca	ccaaaagatg	cacattcaat	aaagttacag	gactctatga	aaaaggatgt	1020
gagtttggtc	tccaatccc	ccagacggag	aaggcttcta	taatgtttgc	acaacatggt	1080
gattctatag	ttgaattctg	tacagaacaa	aaccacaaca	agaagctcc	aaacaagcaa	1140
aatcaaaaa	gcaatctccg	aagcacatgg	gaagtgatcc	gtgattctga	ggactttaag	1200
aaaaccactc	ctatgacaac	acagccacca	aatcccacct	tctcattgct	gcagattgga	1260
caaagaattg	tgtgttttagt	ccttgacaaa	tctggaagca	tggtcgactgg	taaccgcctc	1320
aatcgactga	atcaagcagg	ccagcttttc	ctgctgcaga	cagttgagct	gggttcctgg	1380
gttgggatgg	tgacatttga	cagtgtgcc	catgtacaaa	gtgaactcat	acagataaac	1440
agtggcagtg	acagggacac	actcgccaaa	agattacctg	cagcagcttc	aggaggggacg	1500
tccatctgca	gcgggcttcg	atcggcattt	actgtgatta	ggaagaaata	tccaactgat	1560
ggatctgaaa	tttgtctgct	gacggatggg	gaagacaaca	ctataagtgg	gtgctttaac	1620
gaggtcaaac	aaagtgtgct	catcatccac	acagtgcgtt	tggtggcctc	tgagctcaa	1680
gaactagagg	agctgtccaa	aatgacagga	ggtttacaga	catatgcttc	agatcaagtt	1740
cagaacaatg	gcctcattga	tgcttttggg	gccctttcat	caggaaatgg	agctgtctct	1800
cagcgctcca	tccagcttga	gagtaaggga	ttaaccctcc	agaacagcca	gtggatgaat	1860
ggcacagtga	tcgtggacag	caccgtggga	aaggacactt	tgtttcttat	cacctggaca	1920
acgcagcctc	cccaaactct	tctctgggat	cccagtggac	agaagcaagg	tggttttgta	1980
gtggacaaaa	acacaaaaat	ggcctacctc	caaatcccag	gcattgctaa	ggttggcact	2040
tggaaataca	gtctgcaagc	aagctcacaa	accttgacc	tgactgtcac	gtcccgtgctg	2100
tccaatgcta	ccctgcctcc	aattacagt	acttccaaaa	cgaacaagga	caccagcaaa	2160
ttcccagcc	ctctggtagt	ttatgcaa	attcgccaag	gagcctcccc	aattctcagg	2220
gccagtgtca	cagccctgat	tgaatcagt	aatggaaaaa	cagttacctt	ggaactactg	2280
gataatggag	caggtgtctga	tgctactaag	gatgacgggtg	tctactcaag	gtatttcaca	2340
acttatgaca	cgaatggtag	atacagtgt	aaagtgcggg	ctctgggagg	agtttaacgca	2400
gccagacgga	gagtgatacc	ccagcagagt	ggagcactgt	acatacctgg	ctggattgag	2460
aatgatgaaa	tacaatggaa	tccaccaaga	cctgaaatta	ataaggatga	tgttcaacac	2520
aagcaagtgt	gtttcagcag	aacatcctcg	ggaggctcat	ttgtggcttc	tgatgtccca	2580
aatgctccca	tacctgatct	cttcccacct	ggccaaatca	ccgacctgaa	ggcggaattt	2640
cacgggggca	gtctcattaa	tctgacttgg	acagctcctg	gggatgatta	tgaccatgga	2700
acagctcaca	agtatatcat	tcgaataagt	acaagtattc	ttgatctcag	agacaagttc	2760
aatgaatctc	ttcaagtga	tactactgct	ctcatcccaa	aggaagccaa	ctctgaggaa	2820

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gtctttttgt	ttaaaccaga	aaacattact	tttgaatg	gcacagatct	tttcattgct	2880
attcaggctg	ttgataaggt	cgatctgaaa	tcagaaatat	ccaacattgc	acgagtatct	2940
ttgttttattc	ctccacagac	tccgccagag	acacctagtc	ctgatgaaac	gtctgctcct	3000
tgtcctaata	ttcataatcaa	cagcaccatt	cctggcattc	acatttttaa	aattatgtgg	3060
aagtggatag	gagaactgca	gctgtcaata	gcctagggct	gaatttttgt	cagataaata	3120
aaataaatca	ttcatccttt	ttttgattat	aaaattttct	aaaatgtatt	ttagacttcc	3180
tgtagggggc	gatatactaa	atgtatatag	tacattttata	ctaaatgtat	tcctgtaggg	3240
ggcgatatac	taaatgtatt	ttagacttcc	tgtagggggc	gataaaataa	aatgctaaac	3300
aactgggtaa	a					3311

<210> SEQ ID NO 52

<211> LENGTH: 3067

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

aattaaatta	tgagaattaa	aaagacaaca	ttgagcagag	atgaaaaagg	aagggaggaa	60
aaggtggaaa	agaaaagaag	acaagaagcg	agtagtggtc	tctaacttgc	tcittgaagg	120
atggtctcac	aaagagaacc	ccaacagaca	tcatcgtggg	aatcaaata	agaccagcaa	180
gtacaccgtg	ttgtccttcg	tccccaaaaa	catttttgag	cagctacacc	ggtttgccaa	240
tctctatfff	gtgggcattg	cggttctgaa	ttttatccct	gtggtcaatg	ctttccagcc	300
tgaggtgagc	atgataccaa	tctgtgttat	cctggcagtc	actgccatca	aggacgcttg	360
ggaagacctc	cggaggtaca	aatcggataa	agtcatcaat	aaccgagagt	gcctcatcta	420
cagcagaaaa	gagcagacct	atgtgcagaa	gtgctggaag	gatgtgctgt	tgggagactt	480
catccaaatg	aaatgtcaatg	agattgtccc	agcagacata	ctcctccttt	tttctcttga	540
ccccaatggg	atatgccatc	tggaaaactgc	cagcttggtg	ggagagacaa	acctcaagca	600
aagacgtgtc	gtgaagggtc	tctcacagca	ggaggtacag	ttcgaaccag	agcttttcca	660
caataccatc	gtgtgtgaga	aacccaacaa	ccacctcaac	aaattttaagg	gttatatgga	720
gcatcctgac	cagaccagga	ctggcctttg	ctgtgagagt	cttctgcttc	gaggctgcac	780
catcagaaac	accgagatgg	ctgtttggat	tgtcatctat	gcaggccatg	agacgaaagc	840
catgctgaac	aacagtggcc	cccgggtacaa	acgcagaagc	attgagcggc	gcataaatat	900
agacatcttc	ttctgcattg	ggatcctcat	ccatcatgtg	cttattggag	ctgtagtcca	960
cagcatctgg	aatgggacct	ttgaagaaca	ccctcccttc	gatgtgccag	atgccaatgg	1020
cagcttcctt	cccagtggcc	ttgggggctt	ctacatgttc	ctcacaatga	tcattcctgt	1080
ccagggtgctg	atccccatct	ctttgtatgt	ctccattgag	ctgggtgaagc	tcgggcaagt	1140
gttcttcttg	agcaatgacc	ttgacctgta	tgatgaagag	accgatttat	ccattcaatg	1200
tcgagccctc	aacatcgcag	aggacttggg	ccagatccag	tacatcttct	ccgataagac	1260
ggggaccctg	acagagaaca	agatgggtgt	ccgacgttgc	accatcatgg	gcagcgagta	1320
ttctcaccaa	gaaaatggta	tagaagctcc	caagggtctc	atccctcttt	ctaaaaggaa	1380
ataccctgct	ctcctaagaa	acgaggagat	aaaagacatt	ctcctggctc	tcttagaggc	1440
tgtgtggcat	ttccacaagt	tgtttcctgt	atccctgtgg	tcttccttgt	cacagatcag	1500
ggctgttcca	attacttgta	aactttcatt	tgtttacaaa	ggttagaagt	tatcccatat	1560
gtggttcccc	ttcagctgat	ctttgtctgg	tgccagacaa	agcactttat	gagacgagtt	1620
ttttatctgt	cagcaaatgga	ttggagacat	ttcccaattg	tgtgccagtc	acacaaccaa	1680
ggcttaggaa	ttttctcaggc	cacctttacct	gacatgtctg	ggcaggctctg	tgtctagggtg	1740
catgggtcaga	tttaatacat	ccagaagatg	tcttctattc	taacagatct	cttagcttgt	1800
cactgaggca	aagtttttgat	ttaggagata	gggtataaaa	atgcctggac	tgttaccttg	1860
catggactga	atatgactca	taaaactgat	ctgattccct	cagccatcat	ctgcccact	1920
tggttccccct	ccccaccccc	ccacaacaca	cacacacact	ttctaagaaa	agaaaagaaa	1980
ttcttttttt	tcaatacttt	aagttctggg	atacatgtgc	agaatgtgca	ggtttggtac	2040
ataggtatac	atgtgtcatg	gtggtttgca	gcacccacca	acccatcatc	taccttaggt	2100
atttctccta	atgtatctcc	tcccctagcc	cccaaccccc	cgatgggctc	cagtgtgtga	2160
tgttccccctc	catgtccatg	tgttctcatt	gttcaattcc	cacttatgag	tgagaacatg	2220
cagtatttgg	ttttctgttc	ttgtgttagt	ttgctgatgg	tttctgttc	atccgtgtcc	2280
ctgcaaagga	catgaactca	tcctttttta	tggctgcata	atattccatg	gtgtatatgt	2340
gccacatfff	ctttatccag	tctatcgtct	atgggcactg	gggttggttc	caagtctttg	2400
ctattgtgaa	cagtgtctga	ataaacttac	atgtgcatgt	gtcttttagta	gaatgattta	2460
taatcctttg	ggtatatacc	cagtaatggg	attgtgtgtc	aaatgggtatt	tctgtttcta	2520
gatccttgag	gaatctttgt	cttccacaat	ggttgaacta	atttgtactc	ccaccaacag	2580
tgtaaaagta	ttcctgtttc	tctacatcct	cttcagcatc	tgttgtgtcc	tgacatttta	2640
atgatcacta	ttctcactgg	cgtgagatgt	tatctcattg	tggttttgat	ttgcatttct	2700
ctaataacca	gtaatgatga	gctttttttc	atatgtttgt	tggctgcata	aatgtcttct	2760
tttgagaagt	gtctgttcat	atccttcacc	cattttttga	agaaaacaaa	ctcttaagag	2820
agcagtatct	attccttttga	gtgtgagggg	tggagaaaga	gaaagatgga	gagagtatta	2880

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taagcagctg	tatccccctt	gccatggtga	tagcagacca	ttcacatggg	agcttctggt	2940
ctctttgtaa	taataataag	agccacatta	ccagtactta	gagtatgcta	gttattttta	3000
cacattgtat	cattaaatct	tcaaaacatc	cctatgagtt	agaaacctaa	aaaaaaaaaa	3060
aaaaaaa						3067

<210> SEQ ID NO 53
 <211> LENGTH: 2778
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 53

ctcattttga	tgtctagaat	caggggatcc	aggatcatca	ccaagggtcat	tttcccaggt	60
atggaggggt	ctttctgctt	ctttcttgct	atgcacagct	gctgaggaag	gggctgggag	120
taaagacagt	gaaatgggga	ggaggagtcc	attcaaaccg	agaaacaaag	tgtttggttt	180
ttcttaccct	tggtgtagaa	gctaccaacc	ttttccaaga	aagagggcct	ggcccccttc	240
tcggtctggt	ctgggtgcct	gctgtgcctc	tctggcctcc	cctccgaagg	gcaccattcc	300
ctcgggtgag	tactaccggc	ctgcaccgtg	ttccagtggg	gacagcctga	gaagagagtc	360
tggggcctta	cttcagtacc	ttccttctac	ggcctcacc	tgtgcaaata	atgccacacg	420
ctgcagcctc	cttttcccta	tctataaaat	aaaaatgacc	ctgctctatc	tcactgggct	480
ggcaagaaca	cactgttggt	gccttgacga	cagatgtgct	gaggctgtag	aaagtgcctt	540
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 <211> LENGTH: 1646
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 54

4883-0001 substitute.txt

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<211> LENGTH: 1049

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

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<211> LENGTH: 4815

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

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cagcccaggc	cccgtctacg	ggtagacaga	gccgcatact	cccttaccct	cttcgacgat	180
gagtttgaga	agaaggaccg	gacataccca	gtgggagaga	aacttcgcaa	tgccttcaga	240
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cccaagtaca	agattaaaga	ctacatcatt	cctgacctgc	tcggtggact	cagcggggga	360
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<210> SEQ ID NO 57

<211> LENGTH: 2572

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

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gactatgtct	ggggaaagaa	cggattatgc	cccattaaat	aacaagttgt	gttcaagagt	2040
cagagcagtg	agctcagagg	cccttctcac	tgagacagca	acattttaa	caaaccagag	2100
gaagtatttg	tggaaactcac	tgccctcagt	tgggtaaagg	atgagcagac	aagtcaacta	2160
aagaaaaaag	aaaagcaagg	aggaggggtg	agcaactctg	agcatggagt	tgtttaagtg	2220
ctctctggat	ttgagttgaa	gagcatccat	ttgagttgaa	ggccacaggg	cacaatgagc	2280
tctcccttct	accaccagaa	agtccctggt	caggctctcag	gtagtgcggt	gtggctcagc	2340
tgggttttta	attagcgcac	tctctatcca	acatttaatt	gtttgaaagc	ctccatatag	2400
ttagattgtg	ctttgttaatt	ttgttggtgt	tgctctatct	tattgtatat	gcattgagta	2460
ttaacctgaa	tgttttgtta	cttaaatatt	aaaaaactg	ttatcctaca	aaaaaaccct	2520
caaaggctga	aaataaagaa	ggaagatgga	gacaccctct	gggggtcctc	tc	2572

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<210> SEQ ID NO 58
<211> LENGTH: 1324
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 58
ctttgcagtg gatgcccttg gcaggggtgag cccacaagga gcaatggagc agggcagcgg      60
ccgcttggag gacttccctg tcaatgtgtt ctccgtcact ccttacacac ccagcaccgc      120
tgacatccag gtgtccgatg atgacaaggc gggggccacc ttgctcttct caggcatctt      180
tctgggactg gtggggatca cattcactgt catgggctgg atcaaatacc aagggtgtctc      240
ccactttgaa tggaccacgc tccttgggcc cgtcctgctg tcagttgggg tgacattcat      300
cctgattgct gtgtgcaagt tcaaaatgct ctctgccag ttgtgcaaag aaagtgagga      360
aagggtcccg gactcggaac agacaccagg aggaccatca tttgttttca ctggcatcaa      420
ccaacccatc accttccatg gggccactgt ggtgcagtac atccctcctc cttatggttc      480
tccagagcct atggggataa ataccagcta cctgcagtct gtggtgagcc cctgcggcct      540
cataacctct ggagggggcag cagccgccat gtcaagtcct cctcaatact acaccatcta      600
ccctcaagat aactctgcat ttgtggttga tgagggctgc ctttctttca cggacgggtg      660
aaatcacagg cccaatcctg atgttgacca gctagaagag acacagctgg aagaggaggc      720
ctgtgcctgc ttctctcctc ccccttatga agaaatatac tctctccctc gctagaggct      780
attctgatat aataacacaa tgctcagctc agggagcaag tgtttccgctc attgttacct      840
gacaaccgtg gtgttctatg ttgtaacctt cagaagttac agcagcgccc aggcagcctg      900
acagagatca ttcaaggggg gaaaggggaa gtgggaggtg caatttctca gattggtaaa      960
aattaggctg ggctggggaa attctcctcc ggaacagttt caaattccct cgggtaagaa     1020
atctcctgta taaggttcag gagcaggaat ttacattttt catccaccac cctccccctt     1080
ctctgtagga aggcattggg ggtcacaatt taacccacgc agccaatgga aaaatcacga     1140
cttctgagac tttgggagtt tccacagagg tgagagtcgg gtgggaagga agcaggggaag     1200
agaaagcagg cccagctgga gatttcctgg tggctgtcct tggcccaaaa gcagactcac     1260
taatcccaaa caactcagct gccatctggc ctctctgagg actctgggta ccttaaagac     1320
tata                                             1324

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<210> SEQ ID NO 59
<211> LENGTH: 683
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 59
caggaaagtt cgtgctgcta ggcagaggaa ctgcagcttg ttggcaggtg aaggggagcct      60
gtttagctgt gtccagcaac aacttacgtg gtcctgcttg tgttccaggt gaagcgtctg      120
gccgccgagc agaggaaatca agacctgctc attctttcct cgggggatcc atccagcaat      180
gacatcatct catgctgcca caaggacccc aagtctgggc tgctggggac cagccacgct      240
ccccactgct cattccttca tcctagagac attctgactc tcctccgact gcgctgtgca      300
caggcgtgac aagctctttt acatctcagt ctgcacaact tcaggcactt agcagattga      360
tatgcatcca acaaatattg attgaatatc tgctaaatac ccagtaatgt ttcattgagt      420
attgggtgaa taaaggaatg ctggttcctt ctggccatat taactcctgc acaatactaa      480
gaaaaataaa ttgactagc tgtggaataa tgtgaatccc aatgtcatct attgaaatat      540
tacctgacta ttaaggagta tttatttttg tatcttttct agcaaagtaa ataaaattct      600
taatacagca tatcccttta ttcacggggg gtatgttcca agacccccgg tggatgcctg      660
aaactatgga taataccaga tcc                                             683

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<210> SEQ ID NO 60
<211> LENGTH: 914
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 60
Met Gly Pro Phe Lys Ser Ser Val Phe Ile Leu Ile Leu His Leu Leu
1           5           10           15
Glu Gly Ala Leu Ser Asn Ser Leu Ile Gln Leu Asn Asn Asn Gly Tyr
20           25           30
Glu Gly Ile Val Val Ala Ile Asp Pro Asn Val Pro Glu Asp Glu Thr
35           40           45
Leu Ile Gln Gln Ile Lys Asp Met Val Thr Gln Ala Ser Leu Tyr Leu
50           55           60
Phe Glu Ala Thr Gly Lys Arg Phe Tyr Phe Lys Asn Val Ala Ile Leu
65           70           75           80
Ile Pro Glu Thr Trp Lys Thr Lys Ala Asp Tyr Val Arg Pro Lys Leu

```

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				85					90					95			
Glu	Thr	Tyr	Lys	Asn	Ala	Asp	Val	Leu	Val	Ala	Glu	Ser	Thr	Pro	Pro		
			100					105					110				
Gly	Asn	Asp	Glu	Pro	Tyr	Thr	Glu	Gln	Met	Gly	Asn	Cys	Gly	Glu	Lys		
		115					120					125					
Gly	Glu	Arg	Ile	His	Leu	Thr	Pro	Asp	Phe	Ile	Ala	Gly	Lys	Lys	Leu		
	130					135					140						
Ala	Glu	Tyr	Gly	Pro	Gln	Gly	Lys	Ala	Phe	Val	His	Glu	Trp	Ala	His		
145					150					155					160		
Leu	Arg	Trp	Gly	Val	Phe	Asp	Glu	Tyr	Asn	Asp	Glu	Lys	Phe	Tyr			
				165					170					175			
Leu	Ser	Asn	Gly	Arg	Ile	Gln	Ala	Val	Arg	Cys	Ser	Ala	Gly	Ile	Thr		
		180						185					190				
Gly	Thr	Asn	Val	Val	Lys	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Tyr	Thr	Lys		
		195					200					205					
Arg	Cys	Thr	Phe	Asn	Lys	Val	Thr	Gly	Leu	Tyr	Glu	Lys	Gly	Cys	Glu		
	210					215					220						
Phe	Val	Leu	Gln	Ser	Arg	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Ala		
225					230					235					240		
Gln	His	Val	Asp	Ser	Ile	Val	Glu	Phe	Cys	Thr	Glu	Gln	Asn	His	Asn		
				245					250					255			
Lys	Glu	Ala	Pro	Asn	Lys	Gln	Asn	Gln	Lys	Cys	Asn	Leu	Arg	Ser	Thr		
		260						265					270				
Trp	Glu	Val	Ile	Arg	Asp	Ser	Glu	Asp	Phe	Lys	Lys	Thr	Thr	Pro	Met		
	275						280					285					
Thr	Thr	Gln	Pro	Pro	Asn	Pro	Thr	Phe	Ser	Leu	Leu	Gln	Ile	Gly	Gln		
	290				295						300						
Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly	Ser	Met	Ala	Thr	Gly		
305					310					315					320		
Asn	Arg	Leu	Asn	Arg	Leu	Asn	Gln	Ala	Gly	Gln	Leu	Phe	Leu	Leu	Gln		
				325					330					335			
Thr	Val	Glu	Leu	Gly	Ser	Trp	Val	Gly	Met	Val	Thr	Phe	Asp	Ser	Ala		
		340						345				350					
Ala	His	Val	Gln	Ser	Glu	Leu	Ile	Gln	Ile	Asn	Ser	Gly	Ser	Asp	Arg		
	355						360					365					
Asp	Thr	Leu	Ala	Lys	Arg	Leu	Pro	Ala	Ala	Ala	Ser	Gly	Gly	Thr	Ser		
	370					375					380						
Ile	Cys	Ser	Gly	Leu	Arg	Ser	Ala	Phe	Thr	Val	Ile	Arg	Lys	Lys	Tyr		
385					390					395					400		
Pro	Thr	Asp	Gly	Ser	Glu	Ile	Val	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn		
				405					410					415			
Thr	Ile	Ser	Gly	Cys	Phe	Asn	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Ile		
			420					425					430				
His	Thr	Val	Ala	Leu	Gly	Pro	Ser	Ala	Ala	Gln	Glu	Leu	Glu	Glu	Leu		
		435					440					445					
Ser	Lys	Met	Thr	Gly	Gly	Leu	Gln	Thr	Tyr	Ala	Ser	Asp	Gln	Val	Gln		
	450					455					460						
Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Ser	Ser	Gly	Asn	Gly		
465					470					475					480		
Ala	Val	Ser	Gln	Arg	Ser	Ile	Gln	Leu	Glu	Ser	Lys	Gly	Leu	Thr	Leu		
				485					490					495			
Gln	Asn	Ser	Gln	Trp	Met	Asn	Gly	Thr	Val	Ile	Val	Asp	Ser	Thr	Val		
				500				505					510				
Gly	Lys	Asp	Thr	Leu	Phe	Leu	Ile	Thr	Trp	Thr	Thr	Gln	Pro	Pro	Gln		
	515						520					525					
Ile	Leu	Leu	Trp	Asp	Pro	Ser	Gly	Gln	Lys	Gln	Gly	Gly	Phe	Val	Val		
	530					535					540						
Asp	Lys	Asn	Thr	Lys	Met	Ala	Tyr	Leu	Gln	Ile	Pro	Gly	Ile	Ala	Lys		
545					550					555					560		
Val	Gly	Thr	Trp	Lys	Tyr	Ser	Leu	Gln	Ala	Ser	Ser	Gln	Thr	Leu	Thr		
				565					570					575			
Leu	Thr	Val	Thr	Ser	Arg	Ala	Ser	Asn	Ala	Thr	Leu	Pro	Pro	Ile	Thr		
			580					585					590				

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Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser Pro Leu
      595      600      605
Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser Pro Ile Leu Arg Ala
  610
Ser Val Thr Ala Leu Ile Ile Ser Val Asn Gly Lys Thr Val Thr Leu
625      630      635      640
Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly
      645      650      655
Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser
      660      665      670
Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val
  675      680      685
Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn
  690      695      700
Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp
705      710      715      720
Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser
      725      730      735
Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro
      740      745      750
Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
  755      760      765
Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
  770      775      780
Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
785      790      795      800
Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
      805      810      815
Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
      820      825      830
Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
  835      840      845
Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
  850      855      860
Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
865      870      875      880
Ser Ala Pro Cys Pro Asn Ile His Ile Asn Ser Thr Ile Pro Gly Ile
      885      890      895
His Ile Leu Lys Ile Met Trp Lys Trp Ile Gly Glu Leu Gln Leu Ser
  900      905      910
Ile Ala

```

<210> SEQ ID NO 61

<211> LENGTH: 501

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

```

Met Lys Lys Glu Gly Arg Lys Arg Trp Lys Arg Lys Glu Asp Lys Lys
 1      5      10      15
Arg Val Val Val Ser Asn Leu Leu Phe Glu Gly Trp Ser His Lys Glu
 20      25      30
Asn Pro Asn Arg His His Arg Gly Asn Gln Ile Lys Thr Ser Lys Tyr
 35      40      45
Thr Val Leu Ser Phe Val Pro Lys Asn Ile Phe Glu Gln Leu His Arg
 50      55      60
Phe Ala Asn Leu Tyr Phe Val Gly Ile Ala Val Leu Asn Phe Ile Pro
65      70      75      80
Val Val Asn Ala Phe Gln Pro Glu Val Ser Met Ile Pro Ile Cys Val
      85      90      95
Ile Leu Ala Val Thr Ala Ile Lys Asp Ala Trp Glu Asp Leu Arg Arg
 100      105      110
Tyr Lys Ser Asp Lys Val Ile Asn Asn Arg Glu Cys Leu Ile Tyr Ser
 115      120      125

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Arg	Lys	Glu	Gln	Thr	Tyr	Val	Gln	Lys	Cys	Trp	Lys	Asp	Val	Arg	Val
	130					135					140				
Gly	Asp	Phe	Ile	Gln	Met	Lys	Cys	Asn	Glu	Ile	Val	Pro	Ala	Asp	Ile
145					150					155					160
Leu	Leu	Leu	Phe	Ser	Ser	Asp	Pro	Asn	Gly	Ile	Cys	His	Leu	Glu	Thr
				165					170					175	
Ala	Ser	Leu	Asp	Gly	Glu	Thr	Asn	Leu	Lys	Gln	Arg	Arg	Val	Val	Lys
			180					185					190		
Gly	Phe	Ser	Gln	Gln	Glu	Val	Gln	Phe	Glu	Pro	Glu	Leu	Phe	His	Asn
		195					200					205			
Thr	Ile	Val	Cys	Glu	Lys	Pro	Asn	Asn	His	Leu	Asn	Lys	Phe	Lys	Gly
	210					215					220				
Tyr	Met	Glu	His	Pro	Asp	Gln	Thr	Arg	Thr	Gly	Phe	Gly	Cys	Glu	Ser
225					230					235					240
Leu	Leu	Leu	Arg	Gly	Cys	Thr	Ile	Arg	Asn	Thr	Glu	Met	Ala	Val	Gly
				245					250				255		
Ile	Val	Ile	Tyr	Ala	Gly	His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn	Ser
			260					265					270		
Gly	Pro	Arg	Tyr	Lys	Arg	Ser	Lys	Ile	Glu	Arg	Arg	Met	Asn	Ile	Asp
		275					280					285			
Ile	Phe	Phe	Cys	Ile	Gly	Ile	Leu	Ile	Leu	Met	Cys	Leu	Ile	Gly	Ala
	290					295					300				
Val	Gly	His	Ser	Ile	Trp	Asn	Gly	Thr	Phe	Glu	Glu	His	Pro	Pro	Phe
305					310					315					320
Asp	Val	Pro	Asp	Ala	Asn	Gly	Ser	Phe	Leu	Pro	Ser	Ala	Leu	Gly	Gly
				325					330					335	
Phe	Tyr	Met	Phe	Leu	Thr	Met	Ile	Ile	Leu	Leu	Gln	Val	Leu	Ile	Pro
			340					345					350		
Ile	Ser	Leu	Tyr	Val	Ser	Ile	Glu	Leu	Val	Lys	Leu	Gly	Gln	Val	Phe
		355					360					365			
Phe	Leu	Ser	Asn	Asp	Leu	Asp	Leu	Tyr	Asp	Glu	Glu	Thr	Asp	Leu	Ser
	370					375					380				
Ile	Gln	Cys	Arg	Ala	Leu	Asn	Ile	Ala	Glu	Asp	Leu	Gly	Gln	Ile	Gln
385					390					395					400
Tyr	Ile	Phe	Ser	Asp	Lys	Thr	Gly	Thr	Leu	Thr	Glu	Asn	Lys	Met	Val
				405					410					415	
Phe	Arg	Arg	Cys	Thr	Ile	Met	Gly	Ser	Glu	Tyr	Ser	His	Gln	Glu	Asn
			420					425					430		
Gly	Ile	Glu	Ala	Pro	Lys	Gly	Ser	Ile	Pro	Leu	Ser	Lys	Arg	Lys	Tyr
		435					440					445			
Pro	Ala	Leu	Leu	Arg	Asn	Glu	Glu	Ile	Lys	Asp	Ile	Leu	Leu	Ala	Leu
	450					455					460				
Leu	Glu	Ala	Val	Trp	His	Phe	His	Lys	Leu	Leu	Pro	Val	Ser	Leu	Trp
465					470					475					480
Ser	Ser	Leu	Ser	Gln	Ile	Arg	Ala	Val	Pro	Ile	Thr	Cys	Lys	Leu	Ser
				485					490					495	
Phe	Val	Tyr	Lys	Gly											
			500												

<210> SEQ ID NO 62

<211> LENGTH: 154

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

Met	Gly	Arg	Arg	Ser	Pro	Phe	Lys	Pro	Arg	Asn	Lys	Val	Phe	Gly	Phe
1				5					10					15	
Ser	Tyr	Pro	Trp	Cys	Arg	Ser	Tyr	Gln	Pro	Phe	Pro	Arg	Lys	Arg	Ala
			20					25					30		
Trp	Pro	Pro	Ser	Arg	Val	Trp	Leu	Gly	Ala	Cys	Cys	Ala	Ser	Leu	Ala
		35					40					45			
Ser	Pro	Pro	Lys	Gly	Thr	Ile	Pro	Ser	Gly	Glu	Tyr	Tyr	Arg	Pro	Ala
	50					55				60					
Pro	Ser	Ser	Ser	Gly	Asp	Ser	Leu	Arg	Arg	Glu	Ser	Gly	Ala	Leu	Leu

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65	Gln	Tyr	Leu	Pro	Ser	70	Leu	Ala	Ser	Pro	75	Cys	Ala	Asn	His	Ala	Thr	80	Arg
					85							90					95		
	Cys	Ser	Leu	Leu	Phe	Pro	Ile	Tyr	Lys	100	Ile	Lys	Met	Thr	Leu	110	Leu	Tyr	
				100					105										
	Leu	Thr	Gly	Leu	Ala	Arg	Thr	His	Cys	115	Cys	Cys	Cys	Leu	Ala	120	Asp	Arg	Cys
			115							120					125				
	Ala	Glu	Ala	Val	Glu	Ser	Ala	Phe	Tyr	130	Leu	Val	Gly	Ser	Leu	135	Cys	Ile	
		130					135						140						
	Asn	Ala	Arg	Gly	Ala	Ala	His	Leu	Thr	145	Asp								
						150													

<210> SEQ ID NO 63

<211> LENGTH: 484

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

1	Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	10	Cys	Gly	Leu	Leu	Ala	Ala			
				5											15				
	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	20	Thr	Ala	Val	Leu	Ile	Leu	Gly		
				20					25					30					
	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	35	Gln	Glu	Leu	Lys	Asp	His	Asn		
			35					40					45						
	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	50	Leu	Leu	Ser	Ala	Met	Arg	Glu		
						55				60									
	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	65	Gly	Ser	Leu	Val	Asn	Thr	Val		
						70				75						80			
	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	85	Ile	Thr	Ala	Asn	Ile	Leu	Gln		
					85					90					95				
	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	100	Gln	Glu	Leu	Leu	Val	Lys	Ile		
				100					105						110				
	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	Asn	115	Thr	Pro	Leu	Val	Lys	Thr	Ile		
			115					120						125					
	Val	Glu	Phe	His	Met	Thr	Thr	Glu	Ala	130	Gln	Ala	Thr	Ile	Arg	Met	Asp		
						135				140									
	Thr	Ser	Ala	Ser	Gly	Pro	Thr	Arg	Leu	145	Val	Leu	Ser	Asp	Cys	Ala	Thr		
						150				155							160		
	Ser	His	Gly	Ser	Leu	Arg	Ile	Gln	Leu	165	Leu	His	Lys	Leu	Ser	Phe	Leu		
					165					170						175			
	Val	Asn	Ala	Leu	Ala	Lys	Gln	Val	Met	180	Asn	Leu	Leu	Val	Pro	Ser	Leu		
				180					185						190				
	Pro	Asn	Leu	Val	Lys	Asn	Gln	Leu	Cys	195	Pro	Val	Ile	Glu	Ala	Ser	Phe		
								200						205					
	Asn	Gly	Met	Tyr	Ala	Asp	Leu	Gln	Leu	210	Val	Lys	Val	Pro	Ile	Ser			
							215			220									
	Leu	Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	225	Leu	Leu	Tyr	Pro	Ala	Ile	Lys		
						230				235							240		
	Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	245	Ala	Lys	Leu	Leu	Asp	Ser	Gln		
					245					250						255			
	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	260	Ser	Ala	Ala	Ser	Leu	Thr	Met		
				260					265						270				
	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	275	Leu	Ile	Val	Ser	Gln	Asp	Val		
								280						285					
	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	290	Ser	Pro	Glu	Glu	Phe	Met	Val		
							295			300									
	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	305	Ala	His	Arg	Leu	Lys	Ser	Ser		
						310				315									
	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	320	Asp	Lys	Leu	Gly	Ser	Thr	Gln		
					325					330						335			
	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	340	Pro	Glu	Phe	Phe	Ile	Asp	Gln		
					340				345						350				
	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	Ile	355	Val	Leu	Glu	Val	Phe	Pro	Ser		
								360						365					

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Ser Glu Ala Leu Arg Pro Leu Phe Thr Leu Gly Ile Glu Ala Ser Ser
370 375 380
Glu Ala Gln Phe Tyr Thr Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn
385 390 395 400
Asn Ile Ser Ser Asp Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp
405 410 415
Phe Gln Pro Asp Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser
420 425 430
Ile Leu Leu Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val
435 440 445
Ser Leu Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr
450 455 460
Lys Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
465 470 475 480
Pro Val Ser Gln

```

<210> SEQ ID NO 64

<211> LENGTH: 256

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

```

Met Phe Gln Thr Gly Gly Leu Ile Val Phe Tyr Gly Leu Leu Ala Gln
1 5 10 15
Thr Met Ala Gln Phe Gly Gly Leu Pro Val Pro Leu Asp Gln Thr Leu
20 25 30
Pro Leu Asn Val Asn Pro Ala Leu Pro Leu Ser Pro Thr Gly Leu Ala
35 40 45
Gly Ser Leu Thr Asn Ala Leu Ser Asn Gly Leu Leu Ser Gly Gly Leu
50 55 60
Leu Gly Ile Leu Glu Asn Leu Pro Leu Leu Asp Ile Leu Lys Pro Gly
65 70 75 80
Gly Gly Thr Ser Gly Gly Leu Leu Gly Gly Leu Leu Gly Lys Val Thr
85 90 95
Ser Val Ile Pro Gly Leu Asn Asn Ile Ile Asp Ile Lys Val Thr Asp
100 105 110
Pro Gln Leu Leu Glu Leu Gly Leu Val Gln Ser Pro Asp Gly His Arg
115 120 125
Leu Tyr Val Thr Ile Pro Leu Gly Ile Lys Leu Gln Val Asn Thr Pro
130 135 140
Leu Val Gly Ala Ser Leu Leu Arg Leu Ala Val Lys Leu Asp Ile Thr
145 150 155 160
Ala Glu Ile Leu Ala Val Arg Asp Lys Gln Glu Arg Ile His Leu Val
165 170 175
Leu Gly Asp Cys Thr His Ser Pro Gly Ser Leu Gln Ile Ser Leu Leu
180 185 190
Asp Gly Leu Gly Pro Leu Pro Ile Gln Gly Leu Leu Asp Ser Leu Thr
195 200 205
Gly Ile Leu Asn Lys Val Leu Pro Glu Leu Val Gln Gly Asn Val Cys
210 215 220
Pro Leu Val Asn Glu Val Leu Arg Gly Leu Asp Ile Thr Leu Val His
225 230 235 240
Asp Ile Val Asn Met Leu Ile His Gly Leu Gln Phe Val Ile Lys Val
245 250 255

```

<210> SEQ ID NO 65

<211> LENGTH: 791

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

```

Met Ser Gln Pro Arg Pro Arg Tyr Val Val Asp Arg Ala Ala Tyr Ser
1 5 10 15
Leu Thr Leu Phe Asp Asp Glu Phe Glu Lys Lys Asp Arg Thr Tyr Pro
20 25 30

```


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Val	Gly	Glu	Lys	Leu	Arg	Asn	Ala	Phe	Arg	Cys	Ser	Ser	Ala	Lys	Ile
		35					40					45			
Lys	Ala	Val	Val	Phe	Gly	Leu	Leu	Pro	Val	Leu	Ser	Trp	Leu	Pro	Lys
	50					55					60				
Tyr	Lys	Ile	Lys	Asp	Tyr	Ile	Ile	Pro	Asp	Leu	Leu	Gly	Gly	Leu	Ser
65					70					75					80
Gly	Gly	Ser	Ile	Gln	Val	Pro	Gln	Gly	Met	Ala	Phe	Ala	Leu	Leu	Ala
				85					90					95	
Asn	Leu	Pro	Ala	Val	Asn	Gly	Leu	Tyr	Ser	Ser	Phe	Phe	Pro	Leu	Leu
			100					105					110		
Thr	Tyr	Phe	Phe	Leu	Gly	Gly	Val	His	Gln	Met	Val	Pro	Gly	Thr	Phe
		115					120					125			
Ala	Val	Ile	Ser	Ile	Leu	Val	Gly	Asn	Ile	Cys	Leu	Gln	Leu	Ala	Pro
	130					135					140				
Glu	Ser	Lys	Phe	Gln	Val	Phe	Asn	Asn	Ala	Thr	Asn	Glu	Ser	Tyr	Val
145					150					155					160
Asp	Thr	Ala	Ala	Met	Glu	Ala	Glu	Arg	Leu	His	Val	Ser	Ala	Thr	Leu
				165					170					175	
Ala	Cys	Leu	Thr	Ala	Ile	Ile	Gln	Met	Gly	Leu	Gly	Phe	Met	Gln	Phe
			180					185					190		
Gly	Phe	Val	Ala	Ile	Tyr	Leu	Ser	Glu	Ser	Phe	Ile	Arg	Gly	Phe	Met
		195					200					205			
Thr	Ala	Ala	Gly	Leu	Gln	Ile	Leu	Ile	Ser	Val	Leu	Lys	Tyr	Ile	Phe
	210					215					220				
Gly	Leu	Thr	Ile	Pro	Ser	Tyr	Thr	Gly	Pro	Gly	Ser	Ile	Val	Phe	Thr
225					230					235					240
Phe	Ile	Asp	Ile	Cys	Lys	Asn	Leu	Pro	His	Thr	Asn	Ile	Ala	Ser	Leu
				245					250					255	
Ile	Phe	Ala	Leu	Ile	Ser	Gly	Ala	Phe	Leu	Val	Leu	Val	Lys	Glu	Leu
			260					265					270		
Asn	Ala	Arg	Tyr	Met	His	Lys	Ile	Arg	Phe	Pro	Ile	Pro	Thr	Glu	Met
		275					280					285			
Ile	Val	Val	Val	Val	Ala	Thr	Ala	Ile	Ser	Gly	Gly	Cys	Lys	Met	Pro
	290					295					300				
Lys	Lys	Tyr	His	Met	Gln	Ile	Val	Gly	Glu	Ile	Gln	Arg	Gly	Phe	Pro
305					310					315					320
Thr	Pro	Val	Ser	Pro	Val	Val	Ser	Gln	Trp	Lys	Asp	Met	Ile	Gly	Thr
				325					330					335	
Ala	Phe	Ser	Leu	Ala	Ile	Val	Ser	Tyr	Val	Ile	Asn	Leu	Ala	Met	Gly
			340					345					350		
Arg	Thr	Leu	Ala	Asn	Lys	His	Gly	Tyr	Asp	Val	Asp	Ser	Asn	Gln	Glu
		355					360					365			
Met	Ile	Ala	Leu	Gly	Cys	Ser	Asn	Phe	Phe	Gly	Ser	Phe	Phe	Lys	Ile
	370					375					380				
His	Val	Ile	Cys	Cys	Ala	Leu	Ser	Val	Thr	Leu	Ala	Val	Asp	Gly	Ala
385					390					395					400
Gly	Gly	Lys	Ser	Gln	Val	Ala	Ser	Leu	Cys	Val	Ser	Leu	Val	Val	Met
				405					410					415	
Ile	Thr	Met	Leu	Val	Leu	Gly	Ile	Tyr	Leu	Tyr	Pro	Leu	Pro	Lys	Ser
			420					425					430		
Val	Leu	Gly	Ala	Leu	Ile	Ala	Val	Asn	Leu	Lys	Asn	Ser	Leu	Lys	Gln
		435					440					445			
Leu	Thr	Asp	Pro	Tyr	Tyr	Leu	Trp	Arg	Lys	Ser	Lys	Leu	Asp	Cys	Cys
	450					455					460				
Ile	Trp	Val	Val	Ser	Phe	Leu	Ser	Ser	Phe	Phe	Leu	Ser	Leu	Pro	Tyr
					470					475					480
Gly	Val	Ala	Val	Gly	Val	Ala	Phe	Ser	Val	Leu	Val	Val	Val	Phe	Gln
				485					490					495	
Thr	Gln	Phe	Arg	Asn	Gly	Tyr	Ala	Leu	Ala	Gln	Val	Met	Asp	Thr	Asp
			500					505					510		
Ile	Tyr	Val	Asn	Pro	Lys	Thr	Tyr	Asn	Arg	Ala	Gln	Asp	Ile	Gln	Gly
		515					520					525			
Ile	Lys	Ile	Ile	Thr	Tyr	Cys	Ser	Pro	Leu	Tyr	Phe	Ala	Asn	Ser	Glu

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530	Ile	Phe	Arg	Gln	Lys	Val	535	Ile	Ala	Lys	Thr	Gly	Met	Asp	Pro	Gln	Lys	540
545	Val	Leu	Leu	Ala	Lys	550	Gln	Lys	Tyr	Leu	Lys	555	Gln	Glu	Lys	Arg	560	Arg
				565	Gln	Gln	Arg	Arg	Ser	Leu	Phe	Met	Lys	Thr	Lys	575	Thr	
			580	Glu	Leu	Gln	Gln	Asp	Phe	Glu	Asn	Ala	Pro	Pro	Thr			
		595	Asn	Asn	Gln	Thr	600	Ala	Asn	Gly	Thr	605	Ser	Val	Ser	Tyr		
	610	Thr	Phe	Ser	Pro	Asp	615	Ser	Ser	Ser	Pro	Ala	Gln	Ser	Glu	Pro	Pro	
625	Ala	Ser	Ala	Glu	Ala	Pro	630	Gly	Glu	Pro	Ser	635	Asp	Met	Leu	Ala	Ser	
			645	Thr	Phe	His	650	Thr	Leu	Ile	Leu	Asp	Met	Ser	Gly	Val	655	
			660	Val	Leu	Met	665	Lys	Ala	Leu	Ala	Lys	670	Leu	Ser	Ser		
			675	Gly	Lys	Ile	680	Val	Lys	Val	Phe	Leu	Val	Asn	Ile	His	Ala	
			690	Val	Tyr	Asn	695	Ser	His	Gly	Gly	Val	700	Phe	Glu	Asp	Gly	
705	Leu	Glu	Cys	Lys	His	710	Val	Phe	Pro	Ser	Ile	715	His	Asp	Ala	Val	Leu	
			725	Ala	Arg	Asp	730	Val	Thr	Pro	Gly	His	735	Asn	Phe	Gln	Gly	
			740	Ala	Glu	Leu	745	Ser	Leu	Tyr	Asp	750	Ser	Glu	Glu	Asp	Ile	
			755	Arg	Ser	Tyr	760	Gln	Glu	Met	Phe	765	Gly	Ser	Met	Phe	His	
			770	Ala	Glu	Thr	775	Leu				780						
785						790												

<210> SEQ ID NO 66

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

Met	Glu	Gln	Gly	Ser	Gly	Arg	Leu	Glu	Asp	Phe	Pro	Val	Asn	Val	Phe		
1				5					10					15			
Ser	Val	Thr	Pro	Tyr	Thr	Pro	Ser	Thr	Ala	Asp	Ile	Gln	Val	Ser	Asp		
			20					25					30				
Asp	Asp	Lys	Ala	Gly	Ala	Thr	Leu	Leu	Phe	Ser	Gly	Ile	Phe	Leu	Gly		
		35					40					45					
Leu	Val	Gly	Ile	Thr	Phe	Thr	Val	Met	Gly	Trp	Ile	Lys	Tyr	Gln	Gly		
		50				55					60						
Val	Ser	His	Phe	Glu	Trp	Thr	Gln	Leu	Leu	Gly	Pro	Val	Leu	Leu	Ser		
				70					75						80		
Val	Gly	Val	Thr	Phe	Ile	Leu	Ile	Ala	Val	Cys	Lys	Phe	Lys	Met	Leu		
				85					90					95			
Ser	Cys	Gln	Leu	Cys	Lys	Glu	Ser	Glu	Glu	Arg	Val	Pro	Asp	Ser	Glu		
			100					105					110				
Gln	Thr	Pro	Gly	Gly	Pro	Ser	Phe	Val	Phe	Thr	Gly	Ile	Asn	Gln	Pro		
		115					120					125					
Ile	Thr	Phe	His	Gly	Ala	Thr	Val	Val	Gln	Tyr	Ile	Pro	Pro	Pro	Tyr		
		130				135					140						
Gly	Ser	Pro	Glu	Pro	Met	Gly	Ile	Asn	Thr	Ser	Tyr	Leu	Gln	Ser	Val		
				150					155						160		
Val	Ser	Pro	Cys	Gly	Leu	Ile	Thr	Ser	Gly	Gly	Ala	Ala	Ala	Ala	Met		
			165						170					175			
Ser	Ser	Pro	Pro	Gln	Tyr	Tyr	Thr	Ile	Tyr	Pro	Gln	Asp	Asn	Ser	Ala		
			180					185					190				

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Phe	Val	Val	Asp	Glu	Gly	Cys	Leu	Ser	Phe	Thr	Asp	Gly	Gly	Asn	His
		195					200					205			
Arg	Pro	Asn	Pro	Asp	Val	Asp	Gln	Leu	Glu	Glu	Thr	Gln	Leu	Glu	Glu
	210					215					220				
Glu	Ala	Cys	Ala	Cys	Phe	Ser	Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Tyr	Ser
225					230					235					240
Leu	Pro	Arg													

<210> SEQ ID NO 67
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 67
 acacgaatgg tagatacagt g 21

<210> SEQ ID NO 68
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 68
 atacttgtga gctgttccat g 21

<210> SEQ ID NO 69
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 69
 actgttacct tgcattgact g 21

<210> SEQ ID NO 70
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 70
 caatgagaac acatggacat g 21

<210> SEQ ID NO 71
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 71
 ccatgaaagc tccatgtcta c 21

<210> SEQ ID NO 72
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 72
 agagatggca catattctgt c 21

<210> SEQ ID NO 73

```

<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 73
    atcggctgaa gtcaagcatc g                                21

<210> SEQ ID NO 74
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 74
    tggtcagtga ggactcagct g                                21

<210> SEQ ID NO 75
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 75
    tttctctgct tgatgcactt g                                21

<210> SEQ ID NO 76
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 76
    gtgagcactg ggaagcagct c                                21

<210> SEQ ID NO 77
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 77
    ggcaaatgct agagacgtga c                                21

<210> SEQ ID NO 78
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 78
    aggtgtcctt cagctgccaa g                                21

<210> SEQ ID NO 79
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 79
    gttaagtgtc ctctggattt g                                21

<210> SEQ ID NO 80

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 80
    atcctgattg ctgtgtgcaa g                                     21

<210> SEQ ID NO 81
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 81
    ctcttctagc tggtaacat c                                     21

<210> SEQ ID NO 82
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 82
    ccagcaacaa cttacgtggt c                                     21

<210> SEQ ID NO 83
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 83
    cctttattca cccaatcact c                                     21

<210> SEQ ID NO 84
<211> LENGTH: 2165
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 84
    agaacagcgc agttttgccct cgcgtcacgc agagcctctc cgtggcctcc gcaccttgag      60
    cattaggcca gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc      120
    catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt ttggttctga      180
    gtctcctcaa gctgggatca gggcagtggc aggtgtttgg gccagacaag cctgtccagg      240
    ccttggtggg ggaggacgca gcattctcct gtttctctgt tcctaagacc aatgcagagg      300
    ccatggaagt gcggttcttc aggggccagt tctctagcgt ggtccacctc tacagggacg      360
    ggaaggacca gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg      420
    attctattgc ggagggcgcg atctctctga ggctggaaaa cattactgtg ttggatgctg      480
    gcctctatgg gtgcaggatt agttcccagt ctactacca gaaggccatc tgggagctac      540
    aggtgtcagc actgggctca gttcctctca tttccatcac gggatatggt gatagagaca      600
    tccagctact ctgtcagtc tccggctggt tccccggcc cacagcgaag tggaaaggct      660
    cacaaggaca ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg      720
    atgtggagat ctctctgacc gtccaagaga acgcccggag catatcctgt tccatgcggc      780
    atgctcatct gagccgagag gtggaatcca gggtagagat aggagatacc tttttcgagc      840
    ctatatcgtg gcacctggct accaaagtac tgggaatact ctgctgtggc ctattttttg      900
    gcatgtttgg actgaagatt ttcttctcca aattccagtg taagcgagag agagaagcat      960
    ggcccggtgc cttattcatg gttccagcag ggacaggatg agagatgctc ccacatccag      1020
    ctgcttctct tcttctagtc ctagcctcca ggggccagg cccaaaaaag gaaaatccag      1080
    gcggaactgg actggagaag aaagcacgga caggcagaat tgagagacgc ccggaacac      1140
    gcagtggagg tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg      1200
    aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa gagatttaca      1260
    aggaagagtg tgggtggcttc tcagagtttc caagcaggga aacattactg ggaggtggac      1320
    ggaggacaca ataaaagggtg gcgcgtggga gtgtgccggg atgatgtgga caggaggaag      1380

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gagtacgtga	ctttgtctcc	cgatcatggg	tactgggtcc	tcagactgaa	tggagaacat	1440
ttgtatttca	cattaaatcc	ccgttttatc	agcgtcttcc	ccaggacccc	acctacaaaa	1500
ataggggtct	tcctggacta	tgagtgtggg	accatctcct	tcttcaacat	aaatgaccag	1560
tcccttattt	ataccctgac	atgtcggttt	gaaggcttat	tgaggcccta	cattgagtat	1620
ccgtcctata	atgagcaaaa	tggaactccc	atagtcattc	gcccagtcac	ccaggaatca	1680
gagaaagagg	ccctcttgga	aagggcctct	gcaatcccag	agacaagcaa	cagtgagtcc	1740
tcctcacagg	caaccacgcc	cttcctcccc	aggggtgaaa	tgtaggatga	atcacatccc	1800
acattcttct	ttagggatat	taaggctctc	ctcccagatc	caaagtcccg	cagcagccgg	1860
ccaaggtggc	ttccagatga	aggggggactg	gcctgtccac	atgggagtca	ggtgtcatgg	1920
ctgccctgag	ctgggaggga	agaaggctga	cattacattt	agtttgctct	cactccatct	1980
ggctaagtga	tcttgaaata	ccacctctca	ggtgaagaac	cgtcaggaat	tcccatctca	2040
caggctgtgg	tgtagattaa	gtagacaagg	aatgtgaata	atgcttagat	cttattgatg	2100
acagagtgtg	tcctaattgt	ttgttcatta	tattacactt	tcagtaaaaa	aaaaaaaaaa	2160
aaaaa						2165

<210> SEQ ID NO 85

<211> LENGTH: 347

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 85

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	Ser
1				5				10					15		
Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	Leu	Val
			20					25				30			
Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	Thr	Asn	Ala
		35					40					45			
Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	Ser	Ser	Val	Val
		50				55					60				
His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	Met	Gln	Met	Pro	Gln
65					70					75				80	
Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	Ser	Ile	Ala	Glu	Gly	Arg
				85					90					95	
Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	Val	Leu	Asp	Ala	Gly	Leu	Tyr
			100					105					110		
Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu
		115					120					125			
Leu	Gln	Val	Ser	Ala	Leu	Gly	Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly
		130				135					140				
Tyr	Val	Asp	Arg	Asp	Ile	Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe
145					150					155					160
Pro	Arg	Pro	Thr	Ala	Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser
				165					170					175	
Thr	Asp	Ser	Arg	Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu
			180					185					190		
Ile	Ser	Leu	Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met
		195					200					205			
Arg	His	Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly
		210				215					220				
Asp	Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
225					230					235					240
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys	Ile
				245					250					255	
Phe	Phe	Ser	Lys	Phe	Gln	Cys	Lys	Arg	Glu	Arg	Glu	Ala	Trp	Ala	Gly
			260					265					270		
Ala	Leu	Phe	Met	Val	Pro	Ala	Gly	Thr	Gly	Ser	Glu	Met	Leu	Pro	His
		275					280					285			
Pro	Ala	Ala	Ser	Leu	Leu	Leu	Val	Leu	Ala	Ser	Arg	Gly	Pro	Gly	Pro
		290				295					300				
Lys	Lys	Glu	Asn	Pro	Gly	Gly	Thr	Gly	Leu	Glu	Lys	Lys	Ala	Arg	Thr
305					310					315					320
Gly	Arg	Ile	Glu	Arg	Arg	Pro	Glu	Thr	Arg	Ser	Gly	Gly	Asp	Ser	Gly
				325					330					335	
Ser	Arg	Asp	Gly	Ser	Pro	Glu	Ala	Leu	Arg	Phe					

340

<210> SEQ ID NO 86
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 86
attcatgggt ccagcaggga c 21

<210> SEQ ID NO 87
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 87
gggagacaaa gtcacgtact c 21

<210> SEQ ID NO 88
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 88
tcctggtgtt cgtggtctgc tt 22

<210> SEQ ID NO 89
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 89
gagagtcctg gcttttgtgg gc 22

<210> SEQ ID NO 90
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 90
Gly Ser Ser Asp Leu Thr Trp Pro Pro Ala Ile Lys Leu Gly Cys
1 5 10 15

<210> SEQ ID NO 91
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 91
Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
1 5 10 15

<210> SEQ ID NO 92
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 92
Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu Cys
1 5 10 15

<210> SEQ ID NO 93

```

<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 93
  Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg
  1             5             10

<210> SEQ ID NO 94
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 94
  Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
  1             5             10             15
  Pro Ala Ile Lys Leu Gly
              20

<210> SEQ ID NO 95
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 95
  Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly
  1             5             10

<210> SEQ ID NO 96
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 96
  Gly Ile Gln Glu Gly Gly Phe Cys Phe Arg Ser Thr Arg His Asn Phe
  1             5             10             15
  Asn Ser Met Arg Phe Pro
              20

<210> SEQ ID NO 97
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 97
  Ala Lys Glu Phe Gln Glu Ala Ser Ala Leu Ala Val Ala Pro Arg Ala
  1             5             10             15
  Lys Ala His Lys Ser Gln Asp Ser Leu Cys Val Thr Leu Ala
              20             25             30

<210> SEQ ID NO 98
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 98
  tcctgctcgt cgctctcctg at
                                     22

<210> SEQ ID NO 99
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 99
  tcgctttttg tcgtatttgc
                                     20

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<210> SEQ ID NO 100
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 100
  His Asn Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser
  1          5          10          15

<210> SEQ ID NO 101
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 101
  Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Ala
  1          5          10          15

<210> SEQ ID NO 102
<211> LENGTH: 619
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 102
  Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp Ser His
  1          5          10          15
  Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr Asn His
          20          25          30
  Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg
          35          40          45
  Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu
          50          55          60
  Lys His Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn
  65          70          75          80
  Lys Leu Leu Gln Ile Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr
          85          90          95
  Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg
          100          105          110
  Gly Ser Leu Arg Glu Val Leu Asn Asp Thr Ile Ser Tyr Pro Asp Gly
          115          120          125
  Thr Phe Met Asp Trp Glu Phe Lys Ile Ser Val Leu Tyr Asp Ile Ala
          130          135          140
  Lys Gly Met Ser Tyr Leu His Ser Ser Lys Thr Glu Val His Gly Arg
  145          150          155          160
  Leu Lys Ser Thr Asn Cys Val Val Asp Ser Arg Met Val Val Lys Ile
          165          170          175
  Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro Pro Lys Lys Asp Leu Trp
          180          185          190
  Thr Ala Pro Glu His Leu Arg Gln Ala Asn Ile Ser Gln Lys Gly Asp
          195          200          205
  Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu Ile Ile Leu Arg Lys Glu
          210          215          220
  Thr Phe Tyr Thr Leu Ser Cys Arg Asp Arg Asn Glu Lys Ile Phe Arg
  225          230          235          240
  Val Glu Asn Ser Asn Gly Met Lys Pro Phe Arg Pro Asp Leu Phe Leu
          245          250          255
  Glu Thr Ala Glu Glu Lys Glu Leu Glu Val Tyr Leu Leu Val Lys Asn
          260          265          270
  Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro Asp Phe Lys Lys Ile Glu
          275          280          285
  Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe His Asp Gln Lys Asn Glu
          290          295          300
  Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu Gln Leu Tyr Ser Arg Asn
  305          310          315          320
  Leu Glu His Leu Val Glu Glu Arg Thr Gln Leu Tyr Lys Ala Glu Arg
          325          330          335

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Asp	Arg	Ala	Asp	Arg	Leu	Asn	Phe	Met	Leu	Leu	Pro	Arg	Leu	Val	Val
		340						345					350		
Lys	Ser	Leu	Lys	Glu	Lys	Gly	Phe	Val	Glu	Pro	Glu	Leu	Tyr	Glu	Glu
		355					360					365			
Val	Thr	Ile	Tyr	Phe	Ser	Asp	Ile	Val	Gly	Phe	Thr	Thr	Ile	Cys	Lys
		370				375					380				
Tyr	Ser	Thr	Pro	Met	Glu	Val	Val	Asp	Met	Leu	Asn	Asp	Ile	Tyr	Lys
					390					395					400
Ser	Phe	Asp	His	Ile	Val	Asp	His	His	Asp	Val	Tyr	Lys	Val	Glu	Thr
			405						410					415	
Ile	Gly	Asp	Ala	Tyr	Met	Val	Ala	Ser	Gly	Leu	Pro	Lys	Arg	Asn	Gly
			420					425					430		
Asn	Arg	His	Ala	Ile	Asp	Ile	Ala	Lys	Met	Ala	Leu	Glu	Ile	Leu	Ser
		435					440					445			
Phe	Met	Gly	Thr	Phe	Glu	Leu	Glu	His	Leu	Pro	Gly	Leu	Pro	Ile	Trp
		450				455					460				
Ile	Arg	Ile	Gly	Val	His	Ser	Gly	Pro	Cys	Ala	Ala	Gly	Val	Val	Gly
					470					475					480
Ile	Lys	Met	Pro	Arg	Tyr	Cys	Leu	Phe	Gly	Asp	Thr	Val	Asn	Thr	Ala
				485					490					495	
Ser	Arg	Met	Glu	Ser	Thr	Gly	Leu	Pro	Leu	Arg	Ile	His	Val	Ser	Gly
			500					505					510		
Ser	Thr	Ile	Ala	Ile	Leu	Lys	Arg	Thr	Glu	Cys	Gln	Phe	Leu	Tyr	Glu
		515					520					525			
Val	Arg	Gly	Glu	Thr	Tyr	Leu	Lys	Gly	Arg	Gly	Asn	Glu	Thr	Thr	Tyr
		530				535					540				
Trp	Leu	Thr	Gly	Met	Lys	Asp	Gln	Lys	Phe	Asn	Leu	Pro	Thr	Pro	Pro
					550					555					560
Thr	Val	Glu	Asn	Gln	Arg	Leu	Gln	Ala	Ala	Glu	Phe	Ser	Asp	Met	Ile
				565				570						575	
Ala	Asn	Ser	Leu	Gln	Lys	Arg	Gln	Ala	Ala	Gly	Ile	Arg	Ser	Gln	Lys
			580					585					590		
Pro	Arg	Arg	Val	Ala	Ser	Tyr	Lys	Lys	Gly	Thr	Leu	Glu	Tyr	Leu	Gln
		595					600					605			
Leu	Asn	Thr	Thr	Asp	Lys	Glu	Ser	Thr	Tyr	Phe					
		610				615									

<210> SEQ ID NO 103
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 103
 gctggttaact atcttcctgc 20

<210> SEQ ID NO 104
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of the Artificial Sequence: Oligonucleotide
 <400> SEQUENCE: 104
 gaagaatgtt gtccagaggt 20

<210> SEQ ID NO 105
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 105
 Leu Ile Asn Lys Val Pro Leu Pro Val Asp Lys Leu Ala Pro Leu
 1 5 10 15

```

<210> SEQ ID NO 106
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 106
  Ser Glu Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
   1             5             10             15

<210> SEQ ID NO 107
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 107
  tgttttcaac taccaggggc
                                     20

<210> SEQ ID NO 108
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 108
  tgttggcttt ggcagagtcc
                                     20

<210> SEQ ID NO 109
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 109
  gaggcagagt tcaggcttca ccga
                                     24

<210> SEQ ID NO 110
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 110
  tgttggcttt ggcagagtcc
                                     20

<210> SEQ ID NO 111
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 111
  Thr Gly Met Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val
   1             5             10             15
  Thr ser val Phe Gln Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln
             20             25             30
  Ser Ser Gly Phe Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu
             35             40             45
  Pro Ala Met Leu Gln Ala Val Arg
   50             55

<210> SEQ ID NO 112
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 112

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```

Asp Gln Trp Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val
1      5      10      15
Phe Asn Tyr Gln Gly Leu Trp Arg Ser Cys Val Arg Glu Ser Ser Gly
20      25      30
Phe Thr Glu Cys Arg Gly Tyr Phe Thr Leu Leu Gly Leu Pro Ala Met
35      40      45
Leu Gln Ala Val Arg
50

```

<210> SEQ ID NO 113

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 113

```

Ser Thr Gln Asp Leu Tyr Asn Asn Pro Val Thr Ala Val Phe
1      5      10

```

<210> SEQ ID NO 114

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

```

Asp Met Trp Ser Thr Gln Asp Leu Tyr Asp Asn Pro
1      5      10

```

<210> SEQ ID NO 115

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

```

Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala
1      5      10

```

<210> SEQ ID NO 116

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 116

```

Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly
1      5      10

```

<210> SEQ ID NO 117

<211> LENGTH: 816

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

```

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg      60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac      120
aaccctgtca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt      180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag      240
gcagtgcgag ccctgatgat cgtaggcacg gtcctgggtg ccattggcct cctggtatcc      300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgcca agccaacatg      360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct      420
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc      480
atgggtggga tgggtgcagac tgttcagacc aggtacacat ttgggtgcggc tctgttcgtg      540
ggctgggtcg ctggaggcct cacactaatt ggggtgtgta tgatgtgcat cgcctgccgg      600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt      660
gttgccctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac      720
aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta tccttccaag      780
cacgactatg tgtaatgctc taagacctct cagcac

```

<210> SEQ ID NO 118

<211> LENGTH: 261

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<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 118

```

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1      5      10      15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20      25      30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35      40      45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50      55      60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100      105      110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115      120      125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130      135      140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145      150      155      160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165      170      175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180      185      190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195      200      205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210      215      220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225      230      235      240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245      250      255
Lys His Asp Tyr Val
260

```

<210> SEQ ID NO 119

<211> LENGTH: 227

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

```

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg      60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac      120
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt      180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttcc      227

```

<210> SEQ ID NO 120

<211> LENGTH: 69

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

```

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1      5      10      15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20      25      30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35      40      45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50      55      60
Pro Tyr Phe Thr Ile
65

```

```

<210> SEQ ID NO 121
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 121
aatgagagga aagagaaaac
20

<210> SEQ ID NO 122
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 122
atggtagaag agtaggcaat
20

<210> SEQ ID NO 123
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 123
Glu Lys Trp Asn Leu His Lys Arg Ile Ala Leu Lys Met Val Cys
1 5 10 15

<210> SEQ ID NO 124
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 124
Cys Leu Gly Phe Asn Phe Lys Glu Met Phe Lys
1 5 10

<210> SEQ ID NO 125
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 125
taatgatgaa ccctacactg agc
23

<210> SEQ ID NO 126
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 126
atggacaaat gccctacctt
20

<210> SEQ ID NO 127
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 127
agtgtctggaa ggatgtgcgt gt
22

<210> SEQ ID NO 128

```

```

<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 128
      ttgaggtggt tgttgggttt
                                         20

<210> SEQ ID NO 129
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 129
      agatgtgctg aggctgtaga
                                         20

<210> SEQ ID NO 130
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 130
      atgaaggttg attatttgag
                                         20

<210> SEQ ID NO 131
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 131
      agccgcatac tcccttacct tct
                                         23

<210> SEQ ID NO 132
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 132
      gcagcagccc aaacaccaca
                                         20

<210> SEQ ID NO 133
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 133
      ctgagccgag aggtggaatc
                                         20

<210> SEQ ID NO 134
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 134
      ctctctcgct tacactggaa
                                         20

<210> SEQ ID NO 135

```

```

<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 135
  Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala Leu
  1               5               10

<210> SEQ ID NO 136
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 136
  Ala Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser
  1               5               10               15

<210> SEQ ID NO 137
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 137
  Asn Met Leu Val Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr
  1               5               10               15
  Gly Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly
                20                25                30

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 138
  cgtgagcgct tcgagatggt ccg                                     23

<210> SEQ ID NO 139
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 139
  cctaaccagc tgcccaactg tag                                     23

<210> SEQ ID NO 140
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 140
  ccatgaaagc tccatgtcta                                       20

<210> SEQ ID NO 141
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the Artificial Sequence: oligonucleotide
<400> SEQUENCE: 141
  ggcaaagtgc agagacgtga                                       20

```